



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 160996

TO: Ruixiang Li  
Location: REM/4D75/4C70  
Art Unit: 1646  
Monday, August 08, 2005

Case Serial Number: 10/626398

From: Edward Hart  
Location: Biotech-Chem Library  
REM-1A55  
Phone: 571-272-2512

[edward.hart@uspto.gov](mailto:edward.hart@uspto.gov)

### Search Notes

Examiner Li,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



THE COMPANY

## STIC-Biotech/ChemLib

160986

From: Li, Ruixiang  
Sent: Friday, July 29, 2005 4:02 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.10/626,398

Please do a standard search on:

- (i). SEQ ID NO: 10 against commercial amino acid databases.  
(ii). SEQ ID NO: 7 and 10 against commercial nucleic acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

RECEIVED  
JUL 29 2005  
STIC-Biotech/ChemLib  
(STIC)

\*\*\*\*\*

## STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: 8/2/05  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

## Type of Search

NA#: 1 AA#: 1H1 *reverted to*  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

## Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: OS p/000  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

THE BOSTON PUBLIC LIBRARY

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 17:26:17 ; Search time 238 Seconds  
(without alignments)  
8043.881 Million cell updates/sec

Title: US-10-626-398-7

Perfect score: 1170  
Sequence: 1 atgttgcaataacagctac.....accgcataatccactga 1170

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Issued Patents NA:\*  
2: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfill1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	57.7	1173	3	US-09-414-010-1
2	675	57.7	1173	4	US-09-812-216-1
3	132.2	11.3	1239	4	US-09-891-053-2
4	132.2	11.3	2700	4	US-09-891-053-5
5	123	10.5	1338	3	US-09-165-543-6
6	123	10.5	1953	4	US-09-891-053-26
7	123	10.5	3244	3	US-09-165-543-4
8	110.2	9.4	1335	2	US-08-985-090-3
9	110.2	9.4	1335	3	US-09-165-543-3
10	110.2	9.4	1335	3	US-09-167-354-6
11	110.2	9.4	1335	3	US-09-642-855-6
12	110.2	9.4	1335	3	US-09-642-855-6
13	110.2	9.4	2050	4	US-09-891-053-21
14	110.2	9.4	2665	4	US-09-949-016-5039
15	110.2	9.4	2689	2	US-08-985-090-1
16	110.2	9.4	2689	3	US-09-165-543-1
17	110.2	9.4	2689	3	US-09-167-354-5
18	110.2	9.4	2689	3	US-09-642-855-5
19	110.2	9.4	2689	3	US-09-642-855-5
20	83.2	7.1	1086	2	US-08-985-090-6
21	83.2	7.1	1086	2	US-08-985-090-6
22	83.2	7.1	2218	2	US-08-985-090-4
23	83.2	7.1	2218	2	US-09-165-543-31
24	73.4	6.3	1386	4	US-09-016-434-1339
25	73.4	6.3	1422	4	US-09-826-509-512
26	73	6.2	1581	1	US-08-313-553-8
27	73	6.2	1581	3	US-08-767-993-8

28	73	6.2	1956	1	US-08-313-553-6	Sequence 6, Appl1
29	73	6.2	1956	3	US-08-767-993-6	Sequence 6, Appl1
30	71.2	6.1	1773	4	US-09-826-509-516	Sequence 516, Appl
31	71.2	6.1	1913	4	US-09-016-434-1314	Sequence 1314, Ap
32	69.8	6.0	1056	3	US-09-524-162-1	Sequence 1, Appl1
33	69.4	5.9	1401	4	US-09-826-509-514	Sequence 514, Appl
34	69.4	5.9	2210	4	US-09-016-434-1177	Sequence 1177, Ap
35	69.4	5.9	2210	4	US-09-166-199-1	Sequence 1, Appl1
36	63.8	5.5	1599	4	US-09-826-509-520	Sequence 520, App
37	63.8	5.5	2261	4	US-09-016-434-1176	Sequence 1176, Ap
38	63.2	5.4	601	4	US-09-949-016-177027	Sequence 177027,
39	63.2	5.4	1893	4	US-09-891-053-13	Sequence 13, Appl
40	63.2	5.4	2933	4	US-09-949-016-16801	Sequence 16801, A
41	55.4	4.7	1101	4	US-09-826-509-432	Sequence 432, App
42	55.4	4.7	1554	2	US-08-031-538-8	Sequence 8, Appl1
43	55.4	4.7	1554	4	US-09-016-434-1301	Sequence 1301, Ap
44	55.4	4.7	1730	1	US-07-817-920-1	Sequence 1, Appl1
45	55.4	4.7	1730	1	US-08-117-006-1	Sequence 1, Appl1

## ALIGNMENTS

```
RESULT 1
US-09-414-010-1
; Sequence 1, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Unland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

Query Match      57.7%; Score 675; DB 3; Length 1173;
Best Local Similarity 74.9%; Pred. No. 2.4e-203;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY      8 CAATACAGTACATCGCCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67
      |||
DB      11 CTAATGCAATCAATTCATTCATCACTAGCACTGCTTCTTATGATTTTATGCTT 70
      |||
QY      68 TCTACCTATGCTATTAATGTTAGGAATGCTGCTATTTAGCTTTATTTAGGACA 127
      |||
DB      71 TACTACCTTTGCTATTAATGCTAGGAATGCTTGTGCTATTTAGCTTTTGTGACA 130
      |||
QY      128 GAATCTTACATCACTGAATTAATTTCTTAACTTGGCATTGACATCTTTG 187
      |||
DB      131 AAACCTTACATCACTGAATTAATTTCTTAACTTGGCATTGACATCTTTG 190
      |||
QY      188 TGGGTGATTCCTCATCTCTGTACATACCTTCTGCTGACTTCTGACTTGGAA 247
      |||
DB      191 TGGGTGATTCCTCATCTCTGTACATACCTTCTGCTGACTTCTGACTTGGAA 250
      |||
QY      248 AGCAAGCTTGATTTGGCTATTCATTCAGCATATTTTATGATGAGATCTGTGATA 307
      |||
DB      251 AGCAATCTGTGATTTGGCTATTCATTCAGCATATTTTATGATGAGATCTGTGATA 310
      |||
QY      308 AATATGCTCTCATAGCTACGATCGCTACAGTCAATGCGCTGTGTATAGAG 367
      |||
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311 ACATTGCTCATTCAGCTATGATCGATACCTGTCAAGCTCAAAATGCTGTCTTATAGAA 370  
368 CTCAGCACTCTGGCACTGGAAATATGCTACTCAATGCTGTGCTGTTGGATATCTCT 427  
371 CTCACATATCTGGGCTTGAAGATTTGTTACTGTATGCTGCTGCTGCTGCTGCTGCT 430  
428 TCATGACAAATGGCCGATGATTCGATTTTCACTCTTTGGCAGAAATAGCAATCAAGAT 487  
431 TCTTAGTGAATGGCCAAATGATTTAGTTTCAAGCTTGGAAAGATGAAGTAGATGAAT 490  
488 GTGAACCTGGATTTTAAAAAGTGTACTTTCCTCCCTCAATCATATATTTGAATTC 547  
491 GTGAACCTGGATTTTTCGAAATGATACATCTTGGCAATCATCATATTTTGAATTCG 550  
548 TGATCCCATCTTGTAGTGTCTTATTTTCAAGGCGCCATTTTACTGAGCTGTGGAAGC 607  
551 TGATCCCATCTTGTAGTGTCTTATTTTCAAGGCGCCATTTTACTGAGCTGTGGAAGC 610  
608 GAGAGAACTGAGCAGAGTGTCTCAAGCAGCTGTATCTCCCTCTGACTCTTTCAGCAGTG 667  
611 GTGATCATCTCAAGTGTGCTCAAGGCGCCATCTGAGCTGTGCTGTCTTCCAAACA--- 667  
668 ACCAGGACATCTCTGAGCAACAGAGCCCGATTCAGAGGCGCACTGTGCAAGCAGGAAG 727  
668 TCTGTGACATCTTCAAGAGGTAAGCTATCTTCAAGGAGATCTTCTGTGATGAGAG 727  
728 AAACAATCTGCTCTCTGTTGCTCAAGCAAGTCAAGGAGAAAGAGAGCTCTTGTTCGA 787  
728 AAGTTCCTGCTCTTCTTCAATTCAGAGAGACAGAGAGAAAGATGCTCAATGCTTCT 787  
788 TAAGAGCTCAAGAAACAGCAATGTGATGCTTCCAAATGGGCTTCTCTCCACTGAG 847  
788 CAAGAACCAAGATGATATACATATGCTTCCAAATGGGCTTCTCTCCAAATGAG 847  
848 ATTCCCTGCTCTTCAAGAAAGGAAATATGAACTTTTCAAGAGCAGAGAAATTAAGCA 907  
848 ATTCTGATCTTCAAGAAAGGAAATGATGAACTGCTTGAAGCAGAGAAATTAAGCA 907  
908 AGTCACTGGCAATCTTCAAGAGCTTTCGCAATTTGCTGAGCTCCATATTCAGTACTA 967  
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968 CAGTATCTCAATCTTCTGAAAGGAACTTGAATTAATCAATCTGTGATCAATCTG 1027  
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1088 AAGCTTTTCAAGAGGCTTCTGAAATTAATCTTCTGAAAGGAACTTGAATTAATCAAT 1147  
1088 AAGCTTTTCAAGAGGCTTCTGAAATTAATCTTCTGAAAGGAACTTGAATTAATCAAT 1147  
1148 ACAACCG 1154  
1148 AACACAG 1154

RESULT 2  
US-09-812-216-1  
Sequence 1, Application US/09812216  
Patent No. 6613533  
GENERAL INFORMATION:  
APPLICANT: Behan, Jiang Xu  
APPLICANT: Hedrick, Joseph A.  
APPLICANT: Laz, Thomas M.  
APPLICANT: Monema, Frederick J. Jr.  
APPLICANT: Morse, Kelley L.  
APPLICANT: Umland, Shelby P.  
APPLICANT: Wang, Suke  
TITLE OF INVENTION: Histamine receptor  
FILE REFERENCE: CN01069

CURRENT APPLICATION NUMBER: US/09/812,216  
CURRENT FILING DATE: 2001-03-19  
PRIOR APPLICATION NUMBER: 09/414,010  
PRIOR FILING DATE: 1999-10-07  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patencin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-812-216-1  
Query Match 57.7%; Score 675; DB 4; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 2.4e-203;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;  
8 CAATTAACAGTAAATCCCTTAACATCAATTAATTTCTTTGACATTTTAAATGCT 67  
11 CTAATGACAAATCAATTAATTAATCAATGACCTGCTGATTAATTAATGCT 70  
68 TACTAGTATGCTTAATGTTAGCAATGCTGCTGATTTTACTTTTATTTGAGCA 127  
71 TAGTACCTTTGCTTAATGCTAGAAATGCTTGTGCTATTTTGTGCTGAGCA 130  
128 GAAATCTTGAACATGAAATTAATCTTTTCTTAACTTGGCCATTCAGACTT 187  
131 AAAACCTTGAACATGAAATTAATCTTTTCTTAACTTGGCCATTCAGACTT 190  
188 TGGTGAACATGAAATTTCTTGAATGCTTCTGCTGCTGCTGCTGCTGCTGCT 247  
191 TGGTGAACATGAAATTTCTTGAATGCTTCTGCTGCTGCTGCTGCTGCTGCT 250  
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251 AGCAAGCTTGTGATTTTGGCTCAATTAATGCTATCTTTTGAATGCTGATTA 310  
308 ATATTGCTTCAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATG 367  
311 ACATTGCTTCAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATG 370  
368 CTCAGCACTCTGCACTGCAATGCTAATGCTAATGCTAATGCTAATGCTAAT 427  
371 CTCAGCACTCTGCACTGCAATGCTAATGCTAATGCTAATGCTAATGCTAAT 430  
428 TCATGACAAATGGCCGATGATTCGATTTTCAAGCTTTCGAGAAATAGCAAT 487  
431 TCTTAGTGAATGGCCAAATGATTTGATTTTCAAGCTTTCGAGAAATAGCAAT 490  
488 GTGAACCTGGATTTTAAAAAGTGTACTTTCCTCCCTCAATCATATTTGAATTC 547  
491 GTGAACCTGGATTTTAAAAAGTGTACTTTCCTCCCTCAATCATATTTGAATTC 550  
548 TGATCCCATCTTGTAGTGTCTTATTTTCAAGGCGCCATTTTACTGAGCTGT 607  
551 TGATCCCATCTTGTAGTGTCTTATTTTCAAGGCGCCATTTTACTGAGCTGT 610  
608 GAGAGAACTGAGCAGAGTGTCTCAAGCAGCTGTATCTCCCTCTGACTCTTTCAGCAGTG 667  
611 GTGATCATCTCAAGTGTGCTCAAGGCGCCATCTGAGCTGTGCTGTCTTCCAAACA--- 667  
668 ACCAGGACATCTCTGAGCAACAGAGCCCGATTCAGAGGCGCACTGTGCAAGCAGGAAG 727  
668 TCTGTGACATCTTCAAGAGGTAAGCTATCTTCAAGGAGATCTTCTGTGATGAGAG 727  
728 AAACAATCTGCTCTCTGTTGCTCAAGCAAGTCAAGGAGAAAGAGCTCTTGTTCGA 787  
728 AAGTTCCTGCTCTTCTTCAATTCAGAGAGACAGAGAGAAAGATGCTCAATGCTT 787  
788 TAAGAGCTCAAGAAACAGCAATGTGATGCTTCCAAATGGGCTTCTCTCCACTGAG 847  
788 CAAGAACCAAGATGATATACATATGCTTCCAAATGGGCTTCTCTCCACTGAG 847  
848 ATTCCCTGCTCTTCAAGAAAGGAAATATGAACTTTTCAAGAGCAGAGAAATTAAGCA 907



APPLICANT: Ohba, Masataka  
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
FILE REFERENCE: 06501-083001  
CURRENT APPLICATION NUMBER: US/09/891,053  
CURRENT FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: PCT/JP99/07280  
PRIOR FILING DATE: 1999-12-24  
PRIOR APPLICATION NUMBER: PCT/JP98/05967  
PRIOR FILING DATE: 1998-12-25  
PRIOR APPLICATION NUMBER: JP 11/145661  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 2700  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (351)...(1589)  
NAME/KEY: misc feature  
LOCATION: (1)...(12700)  
OTHER INFORMATION: n = A,T,C or G  
US-09-891-053-5

Query Match 11.3%; Score 132.2; DB 4; Length 2700;  
Best Local Similarity 48.7%; Pred. No. 6,7e-31;  
Matches 523; Conservative 0; Mismatches 528; Indels 24; Gaps 5;

QY 59 TAAATCTTTACTAGCTTTGCTATATATGTTAGGCAATGCTGTGCTCAATTTTACCTTTTA 118  
DB 469 TCATGGCCCTCTCATCTGCGCACAGTACGAGCAACGCGCTGTGCTATGCTCGCTTCG 528  
QY 119 TTGTGGACAGAAATTTAGACATGACATTAATTAATTTTCTTATTTCTTATGCGCATTTGAG 178  
DB 529 TGGCGGATTCAGAGCTTCGACACCAAGAACATTTCTTCTGTCAACCTCGCATCTCG 588  
QY 179 ACTTCTTTGTGGGTGCAATTTGCAATTTCTGTATACATCACTTCTCGCTGACTTAC--T 235  
DB 589 ACTTCTGTGGGTGCTTGTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTTG 648  
QY 236 GAGCTTCTGGAAGACAGCTTGTATTTTGGCTCATTAAGTACTTATTTTATTAAG 295  
DB 649 GAGCTTGTGGCGGCGCTCTGCAAGCTGTGCTGTGATGATCACTACTGTGTGCT 708  
QY 296 CATCTGTATTAATTTGCTCATAGTACGATGCGTACAGCTTCAATTTGCGG 355  
DB 709 CTTGCTTTCAATCTGTAATCTGATGATGATGATGATGATGATGATGATGATGATGATG 768  
QY 356 TGTGTATAGAGCTGACATCTGTGACCTGTGAAATTTGCTACTGATGATGATGATGATG 415  
DB 769 TCTCTTACAGGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 828  
QY 416 GATATTTCTCTTCAATGCAAAATGGGCGGATGATTTGATTTCAAGCTTTGGCAATA 475  
DB 829 GGGTGTGCTCTCTCTGCTGTATGGGCTGCGCATCTGATGGAGATCACTGTGTG 888  
QY 476 GCACTACAG-----AATGTAACCTGATTTTAAAGAGTACTTTGCTC 523  
DB 889 GCACTTCAATCCCGAGGCGCACTCTATGCTGATGATGATGATGATGATGATGATGATGAT 948  
QY 524 TCCCTACATCAATTTTATTTGATTTCTGATCCCATCTGTGATGATGATGATGATGATGATG 583  
DB 949 TCAAGGCTTCAACCTCGAGTTCTTCAAGGCTTCTTCAAGGCTTCTTCAAGGCTTCTTCA 1008  
QY 584 ATATTACTGAGAGCTGTGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643  
DB 1009 GATCTTACCTGAACATCCAGAGGCGGAGGCGGCTTGTGATGATGATGATGATGATGATGAT 1068  
QY 644 TCCCTGTGAGCTTTCAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703  
DB 1069 GCCCAGAACCC---CAACAGATGCGGAGGCTTCCGACCTTCCGACCTTCCGACCTTCC 1124

QY 704 GGGGACTGTGCGACAGCGAAGAAACAACTGCTCTTGTGTTACAGACATGACCGGA 763  
DB 1125 TGGGGCTGTGCGCAAAAGGCGATGGGAGGCGATGCGTTGACAGCTGTGGAGCTTCC 1184  
QY 764 GAAAGAGAGTCTCTTGTTTTTCATTAAGAGCTTACAGAACAGCAATGTATGCTTCCA 823  
DB 1185 TCAAGGGGCACTGAGAGGCGGCTCACTCAAAAGGGGCTCAAGGCCATGACATTTCA 1244  
QY 824 AATGGGCTTCTCTCCACATCAAGTTCCTGCGCTTTCAGAGAGGAGACATATGACAG 883  
DB 1245 GATTCCTGAGAGAGCGCATAGATGTGTGTCAGAGACATC--ACCAAGCGCTTCCGCG 1302  
QY 884 TTTTCAGAGCCAGAAATTTAGCAAGTCACTGCGCATCTTTAGCAAGCTTTTGGCATTT 943  
DB 1303 TGTGCGGGGACAGAGAGGTGCGCAAGTGTGCGCATCATGTGAGCATTTTGGGCTCT 1362  
QY 944 GCTGGCTCCATATTTCACTGACTACATTAATCTACTATTTTCTGAAAGAACTTGA 1003  
DB 1363 GCTGGCGCCGTACACGCTCTTAATGATCATCCAGCTGTGCGCATGCGCGCTGATCC 1422  
QY 1004 CTAAATCAAGCTGTGATCATCTGCTTTTGGCTTCAAGTGTGCAATTCCTTTGTTATC 1063  
DB 1423 CCGATT--ACTGATACAGAGCTTCTTGTGCTTGTGAGGCAACTTGGCGCTTCAAC 1479  
QY 1064 CTTTGTATTCATTTGTGTCAAAACGTTTTCAGAGGCTTTCCTGAAATACT 1118  
DB 1480 CCGTCTCTTACCACTGTGACATCAAGCTTCCGAGAGGCTTTCACCAAGCTTCT 1534

RESULT 5  
US-09-165-543-6  
Sequence 6, Application US/09165543  
Patent No. 6093545  
GENERAL INFORMATION:  
APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman  
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/165,543  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,780  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth A. Hanley  
REGISTRATION NUMBER: 33,505  
REFERENCE/DOCKET NUMBER: NMI-032CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1338 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS



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SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3244 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 778..2112
;
US-09-165-543-4

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Query Match      10.5%; Score 123; DB 3; Length 3244;
Best Local Similarity 54.0%; Pred. No. 6.2e-28;
Matches 305; Conservative 0; Mismatches 245; Indels 15; Gaps 2;

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QY 59 TAATGCTTTTACTAGCTATTCCTATTAATGTTAGCAATGCTGCTCATTTTAACTTTTA 118
DB 896 TCATGGCCCTGCTCATCGTGGCCAGACTGGGCAAGCGCGTGCATGCTCGCTTCG 955
QY 119 TTGCGACAGAAATCTTGAACATGCAATTAATTAATTTTCTTAACTTGGCATTCGAG 178
DB 956 TGGCGAATTCGAGCTTCGCGACCCAGAACTTCTTCTGCTCAACCTCGCATCTCG 1015
QY 179 ACTCTTTGTTGGTGCATTTGCAATTCCTGTCATCATCTTCTCGTGAATTAC--T 235
DB 1016 ACTTCTGCTGGTGGTCCCTTGCATCCATTTGATGATCCTATGCTGACCGGCGCTT 1075
QY 236 GGAATTTCTGGAAGCAAGCTGTGTATTTTGGCTGATTAAGTATCTTTTATGTAAG 295
DB 1076 GGACCTTGGCGCGGGGCTCTGCAAGCTGTGGCTGTGTAAGTAACTTACTGTGTGCT 1135
QY 296 CATCTGTATTAATTTGCTCCATCAGTACGATCGCTACAGTCAATTCGAATGCG 355
DB 1136 CTTGGTCTTCAACATGCTGATCAGTACGATGACCGAATCTCTGCACTCGAGCTG 1195
QY 356 TGTGATATAGAGCTCAGCACTCTGCGACCTGGAAATTTGCTACAGATGCTGCTGTT 415
DB 1196 TCTCTTACAGGGCCGACGAGGGGACAGAGACGGGCGGTTCCGAAGATGGACGTGT 1255
QY 416 GGAATTTCTCTTCAATGCAAAATGSGCGAGATTTCTAATTTCAAGTCTTGGCAGAATA 475
DB 1256 GGGTGTCTGCTTCTCTGCTGATGAGGCTGCGCATCTGATGAGTGGAGTACCTGTGTG 1315
QY 476 GCACTAGAG-----AATGTGAACCTGGAATTTTAAAGAGTAACTTTGCTC 523
DB 1316 GCAATTTCAATCCCGAGGCGCCTGCTATGCTGAGTCTCTTCAACCTGTAATCTTTCA 1375
QY 524 TCCCTACATCAATTAATTTGGAATTCCTGATCCCATCTTGTAGTTGCTTATTTACAGCGCC 583
DB 1376 TCAGGGCTTCACACCTCGAGTTCTTCAAGCGCTTCTCAAGCTTACCTTTCAACCTCA 1435
QY 584 AATATTACTGAGCTGTGGAAGCG 608
DB 1436 GCATCTACCTGAAATCCAGAGGCG 1460

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RESULT 8

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US-08-985-090-3
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silverl
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
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US-08-985-090-3

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Query Match      9.4%; Score 110.2; DB 2; Length 1335;
Best Local Similarity 52.6%; Pred. No. 4.1e-24;
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;

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QY 59 TAATGCTTTTACTAGCTATTCCTATTAATGTTAGCAATGCTGCTCATTTTAACTTTTA 118
DB 119 TCATGGCCCTGCTCATCGTGGCCAGCGTGTGGCCAGCGCTGTGATGCTCGCTTCG 178
QY 119 TTGCGACAGAAATCTTGAACATGCAATTAATTAATTTTCTTAACTTGGCATTCGAG 178
DB 179 TGGCGAATTCGAGCTTCGCGACCCAGAACTTCTTCTGCTCAACCTCGCATCTTCG 238
QY 179 ACTCTTTGTTGGTGCATTTGCAATTCCTGTCATCATCTTCTCGTGAATTAC--T 235
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QY 296 CATCTGTATTAATTTGCTCCATCAGTACGATCGCTACAGTCAATTCGAATGCG 355
DB 359 CTTGCTTCAACATGCTGCTCATCAGTACGACCGCTCTGCTGCTGCTGCTGCTGCTGCT 418
QY 356 TGTGATATAGAGCTCAGCACTCTGCGACCTGGAAATTTGCTACAGATGCTGCTGTT 415
DB 419 TCTCATACGGGGCCGACGAGGGGTGACAGCGGGCGGAGTGGAGAAATGCTGTGTGT 478
QY 416 GGAATTTCTCTTCAATGCAAAATGSGCGAGATTTCTGATTTCAAGTCTTGGCAGAATA 475

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QY 236 CATCTGTGATATAATTGCTCATCATGCTAGATGCTACAGTCTCAATGCGG 355  
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QY 356 TGTGTATAGAGCTCAGCACTGTGCACTGGAATTTGCTACTGATGTGGCTGTT 415  
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Db 419 TCTCATACGGGGCCCGAGGGGAGACCGGGGGGAGTGGGAGAGATGCTGCTGT 478  
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QY 416 GGATATTCCTTCATGACAAATGGGCGCATATTTGTATTTCAACTCTTGGCAGAA 475  
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Db 479 GGGTGTGGCTTCTGTCTGTAGGACGACCATCTGTAGCTGGAGTACTGTCCGGG 538  
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QY 476 GCACTAC-----AGAAATGAACTGTGATTTTAAAAAGTGTACTTGTCTC 523  
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QY 524 TCCCTACATCATTTATTTGAATTCCTGATCCCATCTTGTATTTGCTTATTTCAAGGCC 583  
| | | | |  
Db 599 TCACGGCTTCCACCCCTGGAGTCTTTACGCCCTTCTCTCAGCGTCACTTCTTAACTCA 658  
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QY 584 ATATTACTGAGAGCTGTGGAAGCG 608  
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Db 659 GCATCTACCTGAACATCCAGAGCG 683  
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RESULT 13  
US-09-891-053-21

/ Sequence 21, Application US/09891053  
/ Patent No. 6750322  
/ GENERAL INFORMATION:  
/ APPLICANT: Itadani, Hiraoku  
/ APPLICANT: Takimura, Takao  
/ APPLICANT: Kobayashi, Masahiko  
/ APPLICANT: Tanaka, Ken-ichi  
/ APPLICANT: Hidaka, Yunsuke  
/ APPLICANT: Ohta, Masataka  
/ TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
/ TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS  
/ FILE REFERENCE: 06501-083001  
/ CURRENT APPLICATION NUMBER: US/09/891,053  
/ CURRENT FILING DATE: 2001-09-17  
/ PRIOR APPLICATION NUMBER: PCT/JP99/07280  
/ PRIOR FILING DATE: 1999-12-24  
/ PRIOR APPLICATION NUMBER: PCT/JP98/05967  
/ PRIOR FILING DATE: 1998-12-25  
/ PRIOR APPLICATION NUMBER: JP 11/145661  
/ PRIOR FILING DATE: 1999-05-25  
/ NUMBER OF SEQ ID NOS: 26  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 21  
/ LENGTH: 2050  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (271)...(1629)  
US-09-891-053-21

Query Match 9.4%; Score 110.2; DB 4; Length 2050;  
Best Local Similarity 52.6%; Pred. No. 5.4e-24;  
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;

QY 59 TAATGCTTTACTAGTATTTGCTATATATTTAGCAATGCTGTGATTTAGCTTTTA 118  
| | | | |  
Db 389 TATATGCGCTGCTCATGTCGTCGACCGTGTGGCAACGGGCTGTGATGCTGCGCTTG 448  
| | | | |  
QY 119 TGTGACAGAAATCTTACATGCAAGTATTTACTTTTCTTAACTGGCCATTTGAG 178  
| | | | |  
Db 449 TGGCCGACTCGAGCTTCGCGACCCAGAACAACTTCTTCGCTCAACCTCGCATCTCG 508  
| | | | |  
QY 179 ACTTCTTTGGGTGCAATTTGCAATTCCTCTGTACATCTTCTGCTGAGC---TTACT 235  
| | | | |

Db 509 ACTTCTGTCGGCGGCTTCTGATCCCATGTATGTACCTTACGCTGACAGCGCGCT 568  
| | | | |  
QY 236 GGAATTTGGAAGAGAGTGTGATTTTGGCTCAATTACTATCTTTATATGACG 295  
| | | | |  
Db 569 GAACTTGTGGCCGGGCTTCTGCAAGCTGTGTGTATGTAGATCTGTGTGACCT 628  
| | | | |  
QY 296 CATCTGTGATATAATTGCTCATCATGCTAGATGCTACAGTCTCAATATGCGG 355  
| | | | |  
Db 629 CCTTGGCTTCAACATCGTCTCATAGCTACGACCGCTTCTGTGGTCAACCCGCGG 688  
| | | | |  
QY 356 TGTGTATAGAGCTCAGCACTGTGCACTGGAATTTGCTACTGATGTGGCTGTT 415  
| | | | |  
Db 689 TCTCATACGGGGCCCGAGGGGAGACCGGGGGGAGATGGGAGAGTGTGCTGTGT 748  
| | | | |  
QY 416 GGATATTCCTTCATGACAAATGGGCGCATATTTGTATTTCAACTCTTGGCAGAA 475  
| | | | |  
Db 749 GGGTGTGGCTTCTGTCTGTAGGACGACCATCTGTAGCTGGAGTACTGTCCGGG 808  
| | | | |  
QY 476 GCACTAC-----AGAAATGAACTGTGATTTTAAAAAGTGTACTTGTCTC 523  
| | | | |  
Db 809 GAGAGCTCCATCCCGAGGGGCACTGTATGCGGAGTCTTCTACAACTGTGACTTCTCA 868  
| | | | |  
QY 524 TCCCTACATCATTTATTTGAATTCCTGATCCCATCTTGTATTTGCTTATTTCAAGGCC 583  
| | | | |  
Db 869 TCACGGCTTCCACCCCTGGAGTCTTTACGCCCTTCTCTCAGCGTCACTTCTTAACTCA 928  
| | | | |  
QY 584 ATATTACTGAGAGCTGTGGAAGCG 608  
| | | | |  
Db 929 GCATCTACCTGAACATCCAGAGCG 953  
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RESULT 14

US-09-949-016-5059  
/ Sequence 5059, Application US/09949016  
/ Patent No. 6812339  
/ GENERAL INFORMATION:  
/ APPLICANT: VENTER, J. Craig et al.  
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
/ FILE REFERENCE: CL001307  
/ CURRENT APPLICATION NUMBER: US/09/949,016  
/ CURRENT FILING DATE: 2000-04-14  
/ PRIOR APPLICATION NUMBER: 60/241,755  
/ PRIOR FILING DATE: 2000-10-20  
/ PRIOR APPLICATION NUMBER: 60/237,768  
/ PRIOR FILING DATE: 2000-10-03  
/ PRIOR APPLICATION NUMBER: 60/231,498  
/ PRIOR FILING DATE: 2000-09-08  
/ NUMBER OF SEQ ID NOS: 207012  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 5059  
/ LENGTH: 2665  
/ TYPE: DNA  
/ ORGANISM: Human  
US-09-949-016-5059

Query Match 9.4%; Score 110.2; DB 4; Length 2665;  
Best Local Similarity 52.6%; Pred. No. 6.3e-24;  
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;

QY 59 TAATGCTTTACTAGTATTTGCTATATATTTAGCAATGCTGTGATTTAGCTTTTA 118  
| | | | |  
Db 410 TATATGCGCTGCTCATGTCGTCGACCGTGTGGCAACGGGCTGTGATGCTGCGCTTG 469  
| | | | |  
QY 119 TGTGACAGAAATCTTACATGCAAGTATTTACTTTTCTTAACTGGCCATTTGAG 178  
| | | | |  
Db 470 TGGCCGACTCGAGCTTCGCGACCCAGAACAACTTCTTCGCTCAACCTCGCATCTCG 529  
| | | | |  
QY 179 ACTTCTTTGGGTGCAATTTGCAATTCCTCTGTACATCTTCTGCTGAGC---TTACT 235  
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Db 530 ACTTCTGTCGGCGGCTTCTGATCCCATGTATGTACCTTACGCTGACAGCGCGCT 589  
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QY 236 GGACTTCTGGAAAGCAAGCTGTGATTTTGGCTCAATTACTGACTATCTTTTATGTACAG 295
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Db 590 GGACCTTGGCCGGGGCCCTCTGCAAGCTGTGGCTGTAGTGAAGTCACTGCTGTGCACCT 649
QY 236 CATCTGTATATAATTTGCTCATACGATACGATCGCTACACAGTCACTGCTCAAAATGCCG 355
    |||||
Db 650 CCTTGCCTTCAACATCGTGTCAATCACTGACACCGCTCTGTGCGTCAACCGACGG 709
QY 356 TGTGTATAGAGCTGCACTGTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 415
    |||||
Db 710 TCTCATACCGGGCCGACGAGGTGACACGGCGCGGCGAGTGGGGAAGATGCTGTGTGT 769
QY 416 GGAATTTCTCTTCAATGACAAATGGCGGATATTTGATTTCAACTCTTGGCAGAAATA 475
    |||||
Db 770 GGGTCTGGCTTCTCTGTGTGACGACGACGACGACGACGACGACGACGACGACGACG 829
QY 476 GCACTAC-----AGATGTGAACCTGATTTTAAAGGTACTTTGTCTC 523
    |||||
Db 830 GCACTTCACTCCCGAGGCGCACTGTATGCGAGTCTTCAACATGTGTACTTCTCA 889
QY 524 TCCCTACATCATTTATTTGAAATTCCTGATCCCATCTTTGATGCTTATTTCAAGCGCC 583
    |||||
Db 890 TCAGGCTTCCACCGTGGAGTTCTTTAGGCGCTTCTCTCAAGCTCACTTCTTAACCTCA 949
QY 584 ATATTACTGAGCGCTGTGGAAGCG 608
    |||||
Db 950 GCATCTACCTGAACATCCAGAGCG 974
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## RESULT 15

US-08-985-090-1

Sequence 1, Application US/08985090

Patent No. 5885893

GENERAL INFORMATION:

APPLICANT: Andrew D. J. Goodearl

TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS: LAHIVE &amp; COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/985,090

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jean M. Silveri

REGISTRATION NUMBER: 39,030

REFERENCE/DOCKET NUMBER: MNI-032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2689 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 291..1625

US-08-985-090-1

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Query Match          9.4%; Score 110.2; DB 2; Length 2689;
Best Local Similarity 52.6%; Pred. No. 6.4e-24;
Matches 297; Conservative 0; Mismatches 255; Indels 15; Gaps 2;

QY 59 TAAATCTTTACTAGTATTTGCTATATGTTAGCAATGCTGTCACTTTTATGCTTTTA 118
    |||||
Db 409 TCATGGCCCTCTCATCGTGGCCACGAGTGTGGGCAACGCGTGTGATGCTGCGCTTCG 468
QY 119 TTGTGACAGAAATTTAGATAGTAAATTAATTTTCTTTTCTTAATCTGGCAATTTGAC 178
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Db 469 TGGCCGATCGAGGCTCCGACACCAAGAACAACTTCTCTGCTCAACCTCGCATCTCCG 528
QY 179 AACTCTTTGTGGGTGCAATTTGCAATTTCTCTGTACATCACTTCTCGCTGAC---TACT 235
    |||||
Db 529 ACTTCTGTGTGGGCGCTTGTGCAATCCCACTGTATGTACCTAGCTGTGACAGGCCGCT 588
QY 236 GGACTTCTGGAAGCAAGCTGTGTATTTTGGCTCATTAAGTACTATCTTTTATGTACAG 295
    |||||
Db 589 GGACCTTGGCGCGGCGCTCTGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 648
QY 236 CATCTGTATATAATTTGCTCATACGATACGATCGCTACCAAGTCACTGCAAAATGCCG 355
    |||||
Db 649 CCTTGCCTTCAACATCGTGTCTCATACGCTACGACCGCTTCTGTGAGTCAACCGACG 708
QY 356 TGTGTATAGAGCTGACACTCTGGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 415
    |||||
Db 709 TCTCATACCGGGCCGACGAGGAGTACACGCGCGGCGAGTGGGGAAGATGCTGTGTGT 768
QY 416 GGAATTTCTCTTCAATGACAAATGGCGGATGATTTGATTTCAACTCTTGGCAGAAATA 475
    |||||
Db 769 GGGTGTGGCCCTTCTGTGTGACGACGACATCTTACGCTGAGGAGTACCTGTGCGGG 828
QY 476 GCACTAC-----AGATGTGAACCTGATTTTAAAGGTACTTTGTCTC 523
    |||||
Db 829 GCACTTCACTCCCGAGGCGCACTGTATGCGAGTCTTCTCAACATGTGTACTTCTCA 888
QY 524 TCCCTACATCATTTATTTGAAATTCCTGATCCCATCTTTGATGCTTATTTCAAGCGCC 583
    |||||
Db 889 TCAGGCTTCCACCGTGGAGTTCTTTAGCGCCCTTCTCAAGCTCACTTCTTAACCTCA 948
QY 584 ATATTACTGAGCGCTGTGGAAGCG 608
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Db 949 GCATCTACCTGAACATCCAGAGCG 973
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Search completed: August 5, 2005, 20:19:22  
 Job time : 241 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model1

Run on: August 5, 2005, 15:18:45 ; Search time 5069 Seconds  
(without alignments)  
1184.179 Million cell updates/sec

Title: US-10-626-398-7

Perfect score: 1170  
Sequence: 1 atcgttgccacaataacacagctac.....accgcctcaataccacttga 1170

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
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12: gb\_sy: \*  
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14: gb\_vi: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	675	57.7	1173	6	AR391860 Sequence
4	675	57.7	1173	6	AX109119 Sequence
5	675	57.7	1173	6	AX139113 Sequence
6	675	57.7	1173	6	AX301763 Sequence
7	675	57.7	1173	6	BD015847 Novel pol
8	675	57.7	1173	9	AF307973 Homo sapi
9	675	57.7	1173	9	AF325356 Homo sapi
10	675	57.7	1173	9	AF329449 Homo sapi
11	675	57.7	1173	9	AY008280 Homo sapi
12	675	57.7	1173	9	AY136745 Homo sapi
13	675	57.7	1173	9	HS4298292 Homo sapi
14	675	57.7	1266	6	AX376577 Sequence
15	675	57.7	1300	6	AX301229 Sequence
16	675	57.7	1312	6	BD095598 Novel gua
17	675	57.7	1312	9	AB045370 Homo sapi
18	675	57.7	1316	9	BC069136 Homo sapi
19	675	57.7	3689	6	AX549343 Sequence

20	675	57.7	3689	9	AF312230 Homo sapi
21	671.8	57.4	1227	6	BD097512 Novel gua
22	671.8	57.4	1265	9	AB044934 Homo sapi
23	636.8	54.4	1291	4	AB053300 Sus scrofa
24	616.8	52.7	1593	10	AF358860 Rattus no
25	613	52.4	1538	10	AF358859 Mus muscu
26	444.8	38.0	140555	9	AC007922 Homo sapi
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28	444.8	38.0	167296	2	AP002507 Homo sapi
29	444.8	38.0	169144	2	AC090244 Homo sapi
30	444.8	38.0	184938	2	AP002476 Homo sapi
31	444.8	38.0	193779	2	AP001327 Homo sapi
32	400	34.2	236694	2	AC118386 Rattus no
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36	270	23.1	1326	6	AX451922 Sequence
37	269	23.0	429	6	CQ727333 Sequence
38	155.4	13.3	223	6	AX775381 Sequence
39	138	11.8	721	6	AX230341 Sequence
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42	132.2	11.3	1242	10	AY009371 Rattus no
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#### ALIGNMENTS

RESULT 1  
AF358858 1451 bp mRNA linear ROD 02-SEP-2001  
LOCUS Cavia porcellus histamine H4 receptor mRNA, complete cds.  
DEFINITION AF358858  
ACCESSION AF358858.1 GI:15420532  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Cavia porcellus (domestic guinea pig)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.

REFERENCE  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Comparison of human, mouse, rat, and guinea pig histamine H4  
receptor suggests substantial species variation

JOURNAL  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 1451)

JOURNAL  
REFERENCE Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Direct Submission

JOURNAL  
REFERENCE Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson  
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,  
CA 92121, USA

#### FEATURES

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##### CDS

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/protein\_id="AAK9379.1"  
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TECEPGLKKWYFALPTSLLEPLILVAFPAHLYWSLMKEKLSRCSHVLPSD  
SSSDHGSGCRODPSRATLPARKETTAISGSKSRKSSLSITAYKSNVYASGM  
GFLSHSDSLALQREHIEIPRARKAKSLAILLAALCAIPCARPSITVIVSPPEPL  
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#### ORIGIN

Query Match 100.0%; Score 1170; DB 10; Length 1451;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-284;  
 Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 101 ATGTGGCAAAATTAACATGATCGCTTAACATCAATTAATTTCTTGGACATTTT 160
QY 61 ATGTCTTACTAGCTATTGCTTAATAGTTAGGCAATGTGCTGATTTTACCTTTAT 120
DB 161 ATGTCTTACTAGCTATTGCTTAATAGTTAGGCAATGTGCTGATTTTACCTTTAT 220
QY 121 GTGACAGAAATCTTACATGATGAAATTAATTTTCTTAACTTGGCCATTTGAGAC 180
DB 221 GTGACAGAAATCTTACATGATGAAATTAATTTTCTTAACTTGGCCATTTGAGAC 280
QY 181 TTCTTTGGGGGCAATTGCAATTCCTCTGATACATACCTTCTGCTGACTTACAGACT 240
DB 281 TTCTTTGGGGGCAATTGCAATTCCTCTGATACATACCTTCTGCTGACTTACAGACT 340
QY 241 TCTGAAAGCAAGCTTGTGATTTTGGCTCATTTACTGATCTTTTATGTAAGACATCT 300
DB 341 TCTGAAAGCAAGCTTGTGATTTTGGCTCATTTACTGATCTTTTATGTAAGACATCT 400
QY 301 GTGTATATATTTGCTCTACAGCTACGATCCGTAACAGTCAAGTCAAAATCCCTGTGG 360
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QY 361 TATPAGCTCAGACCTGTGGCACTGGGAAATTTGCTACACATGCTGTGGTGGATTA 420
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QY 421 TTCTCTTCATGACAATGGCCGATGATTTGATTTTCACTTGTGGGAGATAGCACT 480
DB 521 TTCTCTTCATGACAATGGCCGATGATTTGATTTTCACTTGTGGGAGATAGCACT 580
QY 481 ACAGAAATGGAACCTGGATTTTAAAAAGTGATCTTGTCTCTCTACATCATTTATTG 540
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 LOCUS Sequence 1 from patent US 6204017.  
 DEFINITION ARI42850  
 ACCESSION ARI42850  
 VERSION ARI42850.1 GI:15104136  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Unknown.  
 REFERENCE  
 1 (bases 1 to 1173)  
 Behan,J.X., Hedrick,J.A., Laz,T.M., Monsema,F.J., Morse,K.L.,  
 Umland,S.P. and Wang,S.  
 TITLE Polynucleotide encoding a histamine receptor  
 JOURNAL Patent: US 6204017-A 1 20-MAR-2001;  
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 source  
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 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN

Query Match 57.7%; Score 675; DB 6; Length 1173;  
 Best Local Similarity 74.9%; Pred. No. 2.7e-159;  
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

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QY 8 CAATATACAGTACATTCGCTTAACATCAATTAATTTCTTGAATTTTAAATGCTT 67
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Dd		611	GTCATCATCTCAGTAGTGCCMAAGCCAATCTTGAGCTGACTGTCTCTTCCAACA---	667
Oy		668	ACCAACGACACTCCTGCAGACAGGACCCCCGATTCAAGGCGCATCTGCGACAGACGGAAG	727
Dd		668	TCTGTGACACTCATTTGAGAGTAGTAAGTATCTTCAAGGAGATCTTTTCTGTCATGACAG	727
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Dd		728	AAGTTCCTGCACCTCTTCATTTCAAGAGACACAGAGAGAAAGTATGTCATGTTTTCT	787
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Dd		908	AGTACATGGCCATCTCTTACAGGCTTTTGTGCTGGGCTCCATATTCATCTGTGTCA	967
Oy		968	CAGTTATCTACTCATTTTCTCTGGAAGGAAGTAATCAATCAACCTGTATCACTACTG	1027
Dd		968	CAATTTGCTCTTCATTTTATTCCTCAGCAACAGGTCCTTAATCAGTTTGGTATGAATTTG	1027
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Dd		1028	CATTTTGGCTCAGTGGTTCAATTCCTTTGTCAATCCCTTTTGTATTCATTTGTGTACA	1087
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DEFINITION	Sequence 1 from patent US 6613533.				
ACCESSION	AR391860				
VERSION	AR391860.1	GI:40115588			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1173)				
AUTHORS	Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L., Umland,S.P. and Wang,S.				
TITLE	Histamine receptor				
JOURNAL	Patent; US 661353-A 1 02-SEP-2003;				
FEATURES	Location/Qualifiers				
source	1..1173				

**ORIGIN**

Query Match	57.7%	Score 675;	DB 6;	Length 1173;
Best Local Similarity	74.9%	Pred. No. 2.7e-159;		
Matches 859;	Conservative 0;	Mismatches 285;	Indels 3;	Gaps 1;

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DEFINITION AX109119  
ACCESSION AX109119  
VERSION AX109119.1 GI:13924093  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 Behan, J. X., Hedrick, J. A., Laz, T. M., Monema, F. J., Morse, K. L.,  
AUTHORS Umland, S. and Wang, S.  
TITLE Histamine receptor  
JOURNAL Patent: WO 0125432-A 1 12-APR-2001,  
SCHERING CORPORATION (US)  
FEATURES  
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ORIGIN

Query Match 57.7%; Score 675; DB 6; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 2.7e-159;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATPACAGTACCAATCGCCTTAACATCAATTAATTTCTTGAATTTTAAATGCTT 67  
DB 11 CTAATPACAGTACCAATTTTATATCACTAGACACTGCTGTTAGCATTTTATGCTCT 70  
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LOCUS AX139113  
DEFINITION Sequence 1 from Patent EP1096009.  
ACCESSION AX139113  
VERSION AX139113.1 GI:14274791  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 Peter, B. and O'Reilly, M. A.  
AUTHORS G-protein coupled receptor-like polypeptide  
TITLE Patent: EP 1096009-A 1 02-MAY-2001;  
JOURNAL Pfizer Limited (GB); PFIZER INC. (US)  
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Query Match 57.7%; Score 675; DB 6; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 2.7e-159;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

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LOCUS Sequence 1 from Patent WO0185786.  
DEFINITION AX301763  
ACCESSION AX301763  
VERSION AX301763.1 GI:117382844  
KEYWORDS  
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ORGANISM  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 Jones, P. G., Blatcher, M., Wu, S. and Pauesch, M. H.  
AUTHORS Human histamine h 4? receptor  
TITLE Patent: WO 0185786-A 1 15-NOV-2001;  
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Query Match 57.7%; Score 675; DB 6; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 2, 7e-159; Indels 3; Gaps 1;  
Matches 859; Conservative 0; Mismatches 285;  
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LOCUS BD015847  
DEFINITION Novel polypeptide.  
ACCESSION BD015847  
VERSION BD015847.1 GI:22556984  
KEYWORDS JP 2001211889-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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Peter.B. and OlavLee,M.A.  
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PN JP 2001211889-A/1  
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PR 27-OCT-2000 JP 2000329359  
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FT source 1..1173

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Best Local Similarity 74.9%; Pred. No. 2.7e-159;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;  
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Db 1148 AACACAG 1154

## RESULT 8

AF307973 1173 bp mRNA linear PRI 14-NOV-2000  
LOCUS AF307973 Homo sapiens histamine H4 receptor mRNA, complete cds.  
DEFINITION AF307973 AF307973.1 GI:1141732  
VERSION AF307973.1 GI:1141732  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 1173)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Jones, P.G., Wu, S. and Betty, M.  
TITLE Cloning of a novel histamine receptor  
JOURNAL Unpublished  
REFERENCE 2. (bases 1 to 1173)  
Jones, P.G., Wu, S. and Betty, M.  
TITLE Direct Submision  
JOURNAL Submitted (25-SEP-2000) Neuroscience, Wyeth Ayerst, CN8000,  
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Query Match 57.7%; Score 675; DB 9; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 2.7e-159; Indels 3; Gaps 1;  
Matches 859; Conservative 0; Mismatches 285;

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Db 1148 AACACAG 1154

	RESULT 9	
	AFJ25356	
LOCUS	AFJ25356	1173 bp mRNA linear PRI 11-SEP-2001
DEFINITION	Homo sapiens histamine receptor H4 (AXOR35) mRNA, complete cds.	
ACCESSION	AFJ25356	
VERSION	AFJ25356.1	GI:1553202
KEYWORDS		
SOURCE		
ORGANISM	Homo sapiens (human)	
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 1173)	
AUTHORS	Zhu,Y., Michalovich,D., Wu,H.-L., Tan,K.B., Dycko,G.M., Mannan,I.J., Boyce,R., Alston,J., Tierney,L.A., Li,X., Herrity,N.C., Vawter,L., Sarraf,H.M., Ames,R.S., Davenport,C.M., Hsieh,P., Wilson,S., Bergsma,D.J. and Fitzgerald,L.R.	
TITLE	Cloning, expression, and pharmacological characterization of a novel human histamine receptor	
JOURNAL	Mol. Pharmacol. 59 (3), 434-441 (2001)	
MEDLINE	21106320	
PUBMED	11179436	
REFERENCE	2 (bases 1 to 1173)	
AUTHORS	Zhu,Y., Michalovich,D. and Fitzgerald,L.R.	
TITLE	Direct Submission	
JOURNAL	Submitted (30-NOV-2000) GlaxoSmithKline, 709 Swedeland Rd., PO Box 1539, King of Prussia, PA 19406, USA	
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Matches 859; Conservative	0;	Mismatches 285;	Indels 3;	Gaps 1;

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LOCUS	AF329449	1173 bp	mRNA
DEFINITION	Homo sapiens histamine receptor H4 mRNA,	linear	PRI 29-Apr-2001
ACCESSION	AF329449		complete cds.
VERSION	AF329449.1	GI:13876643	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		

REFERENCE 1 (bases 1 to 1173)  
 AUTHORS Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A.,  
 Antnes, J.C., Unland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shin, N.,  
 Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.,  
 and Monma, F.J. Jr.  
 TITLE Cloning and characterization of a novel human histamine receptor  
 J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)  
 JOURNAL MEDLINE  
 PUBMED 11181941  
 REFERENCE 2 (bases 1 to 1173)  
 AUTHORS Monma, F.J. Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and  
 Bayne, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough  
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 USA

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CDS  
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 Matches 889; Conservative 0; Mismatches 285

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 DEFINITION Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.  
 ACCESSION AY008280  
 VERSION AY008280.1 GI:15822540  
 KEYWORDS  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 1173)  
 Nguyen, T., Shapiro, D. A., George, S. R., Setola, V., Lee, D. K.,  
 Cheng, R., Rauber, L., Lee, S. P., Lynch, K. R., Roth, B. L. and  
 O'Dowd, B. F.  
 TITLE Discovery of a novel member of the histamine receptor family  
 JOURNAL MoJ. Pharmacol. 59 (3), 427-433 (2001)  
 MEDLINE 21106319  
 PUBMED 11179435  
 REFERENCE 2 (bases 1 to 1173)  
 Nguyen, T., George, S. R., Lee, D. K., Cheng, R., Lynch, K. R. and  
 O'Dowd, B. F.  
 TITLE Discovery of H4, a Novel Histamine Receptor  
 JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1173)  
 AUTHORS Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and O'Dowd,B.F.  
 TITLE Direct Submission  
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Query Match 57.7%; Score 675; DB 9; Length 1173;  
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 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

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 VERSION AY136745.1 GI:22658472  
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 SOURCE  
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 AUTHORS Puhl,H.L. III, Ikeda,S.R. and Aronstam,R.S.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JUL-2002) cDNA Resource Center, Guthrie Research Institute, One Guthrie Square, Sayre, PA 18840, USA  
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## ORIGIN

Query Match 57.7%; Score 675; DB 9; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 2,7e-159;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAATTAACAGTACATCGCCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67  
DB 11 CTATAGCAACATCAATTTATCATAGCACTGCTGTTACTTTAGCATTTTATGCTT 70  
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ACCESSION AJ298292  
VERSION AJ298292.1 GI:18152452  
KEYWORDS histamine receptor H4; HRH4 gene.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS O'Reilly, M.A.  
TITLE Identification of a histamine H4 receptor on human eosinophils -  
role in eosinophil chemotaxis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1173)  
AUTHORS O'Reilly, M.A.  
TITLE Direct Submission  
JOURNAL Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer  
Ltd, Ramsgate Road, Sandwich, Kent, CT13 9NU, UNITED KINGDOM  
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Query Match 57.7%; Score 675; DB 9; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 2,7e-159;  
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Sequence 5 from Patent WO0200719.
ACCESSION
AX376577.1 GI:19170678
VERSION
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KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Lin,D.C., Zhao,J., Chen,J.L. and Cutler,G.
AUTHORS
Novel receptors
TITLE
Patent: WO 0200719-A 5 03-JAN-2002;
JOURNAL
Tularik Inc. (US)
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Query Match 57.7%; Score 675; DB 6; Length 1266;
Best Local Similarity 74.9%; Pred. No. 2.7e-159;
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992 CAATGTCTCTTCAATTTTATCTCTGACCAAGGTCCTTAATCAAGTTGATTAAGAAATG 1051  
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1148 ACAACCG 1154  
1172 AACACAG 1178

RESULT 15  
AX301229 1300 bp DNA linear PAT 30-NOV-2001  
LOCUS AX301229  
DEFINITION Sequence 1 from Patent WO0185793.  
ACCESSION AX301229  
VERSION AX301229.1 GI:17382320  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Lind, P., Seifritz, T., Vogel, G. and Wood, L.S.  
TITLE G protein-coupled receptors  
JOURNAL Patent: WO 0185793-A 1 15-NOV-2001;  
PHARMACIA & UPJOHN COMPANY (US)  
FEATURES  
source location/Qualifiers  
1..1300

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 57.7%; Score 675; DB 6; Length 1300;  
Best Local Similarity 74.9%; Pred. No. 2,7e-159;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

8 CAATTAACAGTACAAATCGCTTACATCAATTAATTTCTTTGACATTTTATATGCTT 67  
51 CTATATGCAACAAATTAATTAATCACTAGACCTGTGTACTTTAGATTTTATGCTT 110  
68 TACTAGCTATTTGCTATTAATTTGGAAGTGTGGGCTTATTTAGCTTTATTTGAGCA 127  
111 TAGTAGCTTTTGTATTAATTTGGAAGTGTGGGCTTATTTAGCTTTTGTGTGAGCA 170  
128 GAATCTTAGACATGAAAGTAAATTAATTTTCTTAACTTGGCCATTTGACAGCTTCTT 187  
171 AAAACCTTAGACATGAAAGTAAATTAATTTTCTTAACTTGGCCATTTGACAGCTTCTT 230  
188 TGGGTGCAATTTGCAATTTCTCTGTACATACCTTCTGCTGACTTACTGACTTTCGAA 247  
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291 AGGAAATCTGTGTATTTTGGCTCATTAAGTACTGATCTTTTATTTATTTAGTACAGAT 350  
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351 ACATGTCTCATACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 410  
368 CTGAGCACTCTGACACTGGAATTTGCTACTGAGATGCTGCTGTTTGGATATTTCTCT 427  
411 CTCACATATCTGGGCTTGAAGATTTTACTCTGATGAGTGGGCTGTTTGGGCTGCTGCT 470  
428 TCATGACAAATGGGCGGATGATTCGATTTCAAGCTCTTGGGCAATPAGCACTACGAAT 487  
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488 GTGAACTGTGATTTTAAAAAGTGTACTTGTCTCTCCCTACATCAATTAATTTGAATTC 547  
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668 ACCACGACACTCTCTGACAGACAGGACCCGATTCAGAGGCGACTCTGCACAGCAAG 727  
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728 AAACAACTGCTCTCTTGTTCAGACAACTCAAGAGGCAATTTGCTGCTTTTGTTCGA 787  
768 AAGTTCCTGATCTCTTCAATTTCAAGAGAGACAGAGAGAAAGATGATCTCATGTTTCT 827  
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828 CAAGAAACCAAGATGAATGCAATGCAATGCTTCCAAATGGGCTTCTTCCAAATCAG 887  
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888 ATTCTGTAGTCTTTCACCAAGAGGAACATGTGAACCTGCTTGAAGCCAGAGATTAGCCA 947  
908 AGTCACTGGCCATCTTTCAGAGCTTTTGCATTTGCTGGGCTCCATATTCAGTGAATA 967  
948 AGTCACTGGCCATCTTTCAGAGGTTTGTGCTGTTGCTGGGCTCCATATTTCTGTGTA 1007

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Db 1008 CAATTGTCTCTTCATTTTATTCCTCAGCAACAGTCTTAATCAGTTGTATAGAAATTG 1067
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Qy 1028 CCTTTGGCTCCAGTGTGTTCAATTCCTTTGTTAATCCCTTTTGTATCCATTGTGTGACA 1087
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Db 1068 CATTTTGGCTTCAGTGTGTTCAATTCCTTTGTTAATCCCTTTTGTATCCATTGTGTGACA 1127
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Qy 1088 AACGTTTCAGAAAGGCTTCTGAAAAATACTTCTGTGAGAAAGCAATCCACGCCACAC 1147
    |||||
Db 1128 AGCGCTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAAGCAACCTTACCATCACC 1187
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Qy 1148 ACAACCG 1154
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Db 1188 AACACAG 1194
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Search completed: August 5, 2005, 19:13:36  
 Job time : 5073 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 15:08:34 ; Search time 653 Seconds  
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10606.581 Million cell updates/sec

Title: US-10-626-398-7

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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: geneseqn1990a:\*  
3: geneseqn2000a:\*  
4: geneseqn2001a:\*  
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6: geneseqn2002a:\*  
7: geneseqn2002b:\*  
8: geneseqn2003a:\*  
9: geneseqn2003b:\*  
10: geneseqn2003c:\*  
11: geneseqn2003d:\*  
12: geneseqn2004a:\*  
13: geneseqn2004b:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	675	57.7	1170	9	AA55126 Human H4
3	675	57.7	1173	3	AAA46023 Human G P
4	675	57.7	1173	3	AAAD01124 Human GPC
5	675	57.7	1173	4	AAAF83203 Human GPC
6	675	57.7	1173	5	AAH24007 Human his
7	675	57.7	1173	6	ABZ80663 Human his
8	675	57.7	1173	6	ABO78739 Nucleotid
9	675	57.7	1173	6	AAI70980 Human his
10	675	57.7	1173	6	AAI67750 Human his
11	675	57.7	1173	8	ACA93262 Human cdn
12	675	57.7	1173	10	ADG98759 Human GPC
13	675	57.7	1173	10	ABBS57063 Human GPC
14	675	57.7	1173	11	ADJ26922 Human end
15	675	57.7	1173	12	ADG86374 Human end
16	675	57.7	1173	12	ADH88375 Novel hum
17	675	57.7	1173	12	ADP20167 Human G P
18	675	57.7	1173	12	ADQ75073 Human GPC
19	675	57.7	1266	6	ABK12959 DNA seque
20	675	57.7	1300	6	ABA02496 Human G p

21	675	57.7	1312	4	AAH47911 Human G P
22	675	57.7	3689	8	ABZ42573 Human his
23	675	57.7	3689	12	AD005719 Human GPC
24	675	57.7	3689	12	AD029967 Human GPC
25	671.8	57.4	1227	4	AAI66009 Human GPC
26	671.8	57.4	1265	6	AA5898078 Human DNA
27	671.8	57.4	1265	6	AA5898078 Human DNA
28	616.8	52.7	1176	6	AAI70982 Rat histe
29	613	52.4	1176	6	AAI70981 Mouse his
30	613	52.4	1538	12	AD030257 Mouse GPC
31	508.6	43.5	1166	9	AA055124 Human H4
32	438.8	37.5	1103	9	AA055123 Human H4
33	270.8	23.1	540	6	AA5898150 Human G-P
34	270	23.1	1326	6	AA037667 Human G-P
35	155.4	13.3	223	10	AD585481 Farnesyl
36	138	11.8	721	5	AA543459 Human G-P
37	132.2	11.3	1239	2	AAH4570 Rat G-protein
38	132.2	11.3	1239	2	AAH4570 Rat G-protein
39	132.2	11.3	2700	3	AAH4571 G-protein
40	132.2	11.3	2700	3	AAH4571 G-protein
41	124.2	10.6	1311	9	AAI59979 Human H3
42	123	10.5	1338	2	AAH4575 Rat musca
43	123	10.5	1338	12	AD66634 Murine hi
44	123	10.5	1953	3	AAH70638 Rat G-pro
45	123	10.5	2761	10	ABR42301 Toxicity

#### ALIGNMENTS

RESULT 1  
AAI70983  
ID AAI70983 standard; cDNA, 1170 BP.  
AC AAI70983;  
XX  
XX  
DT 18-MAR-2002 (first entry)  
XX  
XX  
DE Guinea pig histamine H4 receptor cDNA.  
KW Histamine H4 receptor; guinea pig; antiaesthetic; antiallergenic;  
KW antiinflammatory; cardiac; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy; ss.  
XX  
OS Cavia porcellus.  
XX  
PN W0200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001, 2001MO-US005914.  
XX  
PR 31-MAY-2000, 2000US-0208260P.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;  
XX  
XX WPI, 2002-114339/15.  
XX P-PSDB; AAM50567.  
XX  
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
XX the protein, useful in gene therapy for treating diseases where it is  
XX beneficial to elevate mammalian histamine H4 receptor activity.  
XX  
XX Claim 4, Fig 6B; 92pp; English.  
XX  
XX The present sequence is that of a cDNA clone encoding guinea pig  
XX histamine receptor of the H4 subtype. The cDNA was isolated from a bone  
XX marrow cDNA library. It shows 75.6% homology to the human H4 receptor  
XX coding region. The invention provides mammalian (human, mouse, rat and  
XX guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-  
XX 83) and polypeptides (see AAM50564-67). The nucleic acids have been

expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the mammalian histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity

Sequence 1170 BP; 301 A; 286 C; 221 G; 362 T; 0 U; 0 Other;

Query Match 100.0%; Score 1170; DB 6; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 ATGCTTTACTAGTATTGCTAATATGTTAGCAATGTCGTGATTTTACTTTTATTT 120
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DB 421 TTCTCTCTCATGACAAATGCGCCGAGATTTGATTTTGAAGCTCTTGCGCAATAGCACT 480
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DB 781 TTTTCATTAAGAGCTTACAAAGACGAATGTGATCGCTTCCAAATGGAGCTTCCCTCC 840

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QY 961 CTGACTACAGTATCTACTCAATTTTCTGAAAGAACTTGAATCAACCTGATAC 1020
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DB 1021 CATACCTGCTTTTGGCTCAGTGGTCAATTCCTTTGTAATCCCTTTTGTATCATTTG 1080
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DB 1141 CCACCAACAACCGCTCAATATCCACTTGA 1170

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RESULT 2  
AADS5126  
ID AADS5126 standard; DNA; 1170 BP.

AC AADS5126;  
DT 07-AUG-2003 (first entry)  
XX  
XX  
DE Human H4 receptor wild-type DNA #2.

XX Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;  
XX atopic dermatitis; stroke; myocardial infarction; migraine; allergy;  
XX chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;  
XX rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;  
XX asthma; receptor; gene; ds.

OS Homo sapiens.

XX  
XX Key Location/Qualifiers  
FH 1..1170  
FT CDS  
FT /\*tag= a  
FT /product= "Human H4 protein"  
FT /note= "CDS does not include stop codon"  
FT /partial

WO2003020907-A2.

13-MAR-2003.

PD 30-AUG-2002; 2002WO-US027891.

PF 31-AUG-2001; 2001US-0316762P.

PR 13-NOV-2001; 2001US-0332697P.

XX (MERI ) MERCK & CO INC.

XX Gallagher MJ, Yates SL;

XX WPI; 2003-290186/28.

DR P-PSDB; AAB36417.

XX Novel splice variants of human H4 histamine receptor, H4b and H4c, useful  
XX for identifying agonists or antagonists of the receptor which are useful  
XX for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.

PS Disclosure; Page 56-58; 31pp; English.

XX The invention relates to splice variants of human H4 histamine receptor.

CC H4b and H4c. The invention is useful for identifying an agonist, antagonist or inverse agonist of a mammalian histamine receptor. The CC agonist, antagonist or inverse agonist of H4b and H4c is useful for treating inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease, or psoriasis. The present sequence is human H4 receptor DNA

Sequence 1170 BP; 292 A; 245 C; 231 G; 402 T; 0 U; 0 Other;

Query Match 57.7%; Score 675; DB 9; Length 1170;  
Best Local Similarity 74.9%; Pred. No. 3,5e-190;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

```

QY 8 CAAATAACAGTACAAATGCGCTTAACATCAATTAATAATCTTGACATTTTAAATGCTT 67
DB 11 CTATATGCAACATCAATTTATCACTAGACACTGCTGTACTTACAGCAATTTTAAATGCTT 70
QY 68 TACTAGCTATGCTATATATGTTAGGCAATGCTGGTCATTTTAACTTTTAAATGTTGACA 127
DB 71 TGTAGCTTTTGTCTATATATGCTAGAAATGCTTGGTCATTTTAACTTTTAACTTTTAACT 130
QY 128 GAAATTTTACATCGAAGTAATTAATCTTTTCTTAACTTGGCCATTTGACACTTCTTGG 187
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QY 248 AGCAACCTTGTATTTTGGCTCATTTACTGACTATCTTTTATGTACAGACTGTGTATA 307
DB 251 AGGAATCTGTATTTTGGCTCATCTACTGACTATCTTTTATGTACAGACTGTGTATA 310
QY 308 AATATGCTCTCATGCTACGATGCTGCTACGACTGCTGCTGCTGCTGCTGCTGCTGCTG 367
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DB 431 TCTTATGTAATGGGCGCAATATCTTATTTCAAGACTTTGGCAGAAATAGCACTACAGAA 490
QY 488 GTGAACCTGGATTTTAAAAAGTGTACTTGTCTCTCCCTACATCATTTATGGAATTC 547
DB 491 GTGAACCTGGATTTTAAAAAGTGTACTTGTCTCTCCCTACATCATTTATGGAATTC 550
QY 548 TGAATCCCATCTTGTATGTTAGTTTATTTTCAAGCCCATATTTACTGAGCTGTGGAAGC 607
DB 551 TGAATCCCATCTTGTATGTTAGTTTATTTTCAAGCCCATATTTATTTGAGCTGTGGAAGC 610
QY 608 GAGAGAAATGAGCAGAGTGGCTGAGCACTCTGTAATCTCCCTGTAATCTTTCAGCAGNTG 667
DB 611 GTGATATCTCTCAATAGTGTGCAAGCAATCTTGAATGCTGTCTCTTCCAAACA--- 667
QY 668 ACCACGAGCACTCTGAGCAGAGCACTCCGATTTCAAGGGGCACTTGCAGACGGAAG 727
DB 668 TCTGTGAGCACTCTGAGCAGAGCACTCTCAAGAGATATCTTTTTCGATTCAGCAG 727
QY 728 AAACAATGCTCTCTGTTGTTAGCAAGTCAAGGGAAGAGACAGTCTTTTTCCTCA 787
DB 728 AAGTCTCTGATCTTTTCAATTCAGAGAGACAGAGGAAAGAAATAGTCTATGTTTTCCT 787
QY 788 TAAGAGCTTCAAGAAACAGCAATGTGATCGCTTCAAAATGGGCTTCTCCCACTCAG 847
DB 788 CAAAGAACAAAGATAGATAGCAATATCAATTCCTTCCAAATGGGCTTCTTCCCACTCAG 847
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QY 968 CAGTTATCTACTGATTTTCTCTGAAAGAACTTGAATCAATCACTGCTGCTGCTGCTG 1027
DB 968 CAGTTATCTACTGATTTTCTCTGAAAGAACTTGAATCAATCACTGCTGCTGCTGCTG 1027
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DB 1028 CATTGTGGCTTCAAGTGTCTCAATCTCTTGTATATCCCTTTTGTATCCATTTGTGCACA 1087
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DB 1088 AGCGCTTTCAGAGGCTTCTGAAATATCTTCTGAGAGAGCAATCCAGCTTACATCAC 1147
QY 1148 ACAACCG 1154
DB 1148 ACAACAG 1154

RESULT 3
AAA46023
ID AAA46023 standard; cDNA; 1173 BP.
XX
XX AAA46023:
AC 22-AUG-2000 (first entry)
XX
XX
DE Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.
XX
XX Human: G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;
XX
XX Homo sapiens.
XX
XX PN WO200022131-A2.
XX
XX 20-APR-2000.
XX
XX 13-OCT-1999; 99WC-US024065.
XX
PR 13-OCT-1999; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123945P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 28-MAY-1999; 99US-0137567P.
PR 28-JUN-1999; 99US-0141448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.

```







DT 10-AUG-2001 (first entry)  
 XX Human G protein-coupled receptor AXOR35 cDNA.  
 DE  
 XX  
 XX AXOR35; human; G protein-coupled receptor; 7TM receptor;  
 KM histamine H3 receptor homologue; infection; viral; bacterial; fungal;  
 KM protozoan; HIV-1; HIV-2; palm; cancer; diabetes; obesity; anorexia;  
 KM bulimia; osteoporosis; asthma; allergy; urinary retention;  
 KM acute heart failure; hypotension; hypertension; angina pectoris;  
 KM myocardial infarction; stroke; ulcer; migraine; vomiting;  
 KM psychotic disorder; neurological disorder; anxiety; schizophrenia;  
 KM manic depression; bipolar disorder; depression; delirium; dementia;  
 KM Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;  
 KM macrophage; eosinophil; neutrophil; function modulation;  
 KM autoimmune disorder; pulmonary disorder; gene therapy; vaccine;  
 KM drug screening; signal transduction; transgenic animal; drug discovery;  
 KM sb.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT 1.1173  
 FT CDS /tag= a  
 FT /product= "Human AXOR35"  
 XX /note= "G protein-coupled receptor"  
 XX  
 PN MO200133221-A1.  
 XX  
 XX 10-MAY-2001.  
 PD  
 XX  
 XX 26-OCT-2000; 2000MO-US029461.  
 PF  
 XX  
 XX 02-NOV-1999; 99US-00431898.  
 PR 03-FEB-2000; 2000US-00497790.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;  
 PI Michaelovich D, Morrow DM, Zhu Y;  
 PT WPI; 2001-316464/33.  
 DR P-PSDB; AAB73622.  
 XX  
 XX Novel G-protein coupled receptor polypeptide and polynucleotide for  
 PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological  
 PT disorders and for identifying modulators useful for treating asthma.  
 XX  
 XX  
 PS Claim 2; Page 49-50; 54pp; English.

CC function of lymphocytes, macrophages, eosinophils or neutrophils in  
 CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also  
 CC useful for diagnosing or determining susceptibility of an individual to a  
 CC disease via the detection of abnormal levels of protein or mRNA, or via  
 CC the detection of mutations in the corresponding gene. AXOR35 proteins are  
 CC also useful for inducing an immunological response in a mammal against  
 CC the above diseases, and for antibody production. AXOR35 nucleotides are  
 CC also useful as diagnostic reagents, in chromosome localisation and tissue  
 CC expression studies, and for producing transgenic animals useful in drug  
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35  
 CC protein or fragments thereof, and are also useful for treating conditions  
 CC associated with the expression of the AXOR35 protein. The present  
 CC sequence represents cDNA encoding human AXOR35  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Query Match 57.7%; Score 675; DB 5; Length 1173;  
 Best Local Similarity 74.9%; Pred. No. 3,5e-190;  
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;  
 QY 8 CAAATTAACGTACATCGCCTTAACATCAATTAATTTCTTGAGATTTTATGCTT 67  
 DB 11 CTAAATGACAAATCAATTTATCTAAGACCTGCTTACTTAAAGCAATTTTATGCTT 70  
 QY 68 TACTAGCTTTGCTAATATGTTAGCAATGTCGTGTCATTTAGCTTTATTTGGACA 127  
 DB 71 TAGTACCTTTTGGTAAATGCTAATGCAAAATGCTTTGGTCAATTTAGCTTTTGGTGA 130  
 QY 128 GAAATCTTAAACATGCAAGTAAATTAATTTCTTAACTTGGCATTGCAAGCTTTCTT 187  
 DB 131 AAAACCTTAAACATGCAAGTAAATTTTCTTAACTTGGCATTGCAAGCTTTCTT 190  
 QY 188 TGGTGCAATTTGCAATTTCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTT 247  
 DB 191 TGGTGCAATTTGCAATTTCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTT 250  
 QY 248 AGCAAGCTTGTATTTGGCTCATCTACTACTACTACTACTACTACTACTACTACTACT 307  
 DB 251 AGCAAGCTTGTATTTGGCTCATCTACTACTACTACTACTACTACTACTACTACTACT 310  
 QY 308 AATATGCTTCAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATG 367  
 DB 311 AATATGCTTCAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATG 370  
 QY 368 CTGACGATCTTGGCAGCTGGAATTTGCTAATGCTAATGCTAATGCTAATGCTAATG 427  
 DB 371 CTGACGATCTTGGCAGCTGGAATTTGCTAATGCTAATGCTAATGCTAATGCTAATG 430  
 QY 428 TCATGCAATATGGCGGATGATCTGATTTCAAGCTTTGGCAGATATGACATACAGAA 487  
 DB 431 TCATGCAATATGGCGGATGATCTGATTTCAAGCTTTGGCAGATATGACATACAGAA 490  
 QY 488 GTGAACTGGATTTTAAAAAGTGTACTTGTCTCTCCATCATATTAATTTGAAATTC 547  
 DB 491 GTGAACTGGATTTTAAAAAGTGTACTTGTCTCTCCATCATATTAATTTGAAATTC 550  
 QY 548 TGAATCCCATCTTGTAGTTGCTTATTTCAAGGCGCATATTTAATGAGGCTTGAAGC 607  
 DB 551 TGAATCCCATCTTGTAGTTGCTTATTTCAAGGCGCATATTTAATGAGGCTTGAAGC 610  
 QY 608 GAGAGAAATGAGCAGATGCTCAGGCACTGTATCTCCCTGTGACTCTTCAGCAGTG 667  
 DB 611 GAGAGAAATGAGCAGATGCTCAGGCACTGTATCTCCCTGTGACTCTTCAGCAGTG 667  
 QY 668 ACCACGAACTCTGCAAGACGAGCCCGATTTCAAGGCGCATATTTAATGAGGCTTGA 727  
 DB 668 TCTGTGAACTATTTCAAGGAGTATCTTCAAGGAGATCTTTCGACATGACAG 727  
 QY 728 AAACAACTGCTCTCTGTTGTTAGCAAGATGCAAGGAGGAGGAGGAGGAGGAGGAGG 787  
 DB 728 AAATCTTCTCTCTCTGTTGTTAGCAAGATGCAAGGAGGAGGAGGAGGAGGAGGAGG 787  
 QY 788 TAAGAGCTTAAAGAACAGCAATGATGATGCTTCAAAATGGGCTTCTCTCCACTCAG 847

```
Db      768 CAAGAACCAAGATGATAGCATACATATGCTTCCAAAATGGGTTCTTCCCATACAG 847
Oy      848 ATTCCCTGGCTCTTACAGCAAGGAAACATATGCACTTTTCAGACCAAGAAATTAGCCA 907
Db      848 ATTCTGTAGCTCTTACCAAGGAAACATGTTGMACTGTTAGACCCAGAGATTAGCCA 907
Oy      908 AGTCATCGGCATCTCTTAGCAGCTTTGGCCATTGCTGGGCTCCATTTACTGACTA 967
Db      908 AGTCATCGGCATCTCTTAGGAGGTTTGGCTGTTGGCGGCTCCATTTCTCTGTCA 967
Oy      968 CAGTATCTACTCATTTTCTCTGAAAGAACTTACTTAAACACCTGTTCCATCTG 1027
Db      968 CATTGTCTCTTCAATTTATTTCTCGAACAAGCTCTTAAATCAGTTGGATAGAAATTG 1027
Oy      1028 CTTTGGCTCCAGTGTTCATTCCTTTGTTAATCCCTTTTGTATCATTGTGTACA 1087
Db      1028 CATTTTGGCTTACGTGTTCATTCCTTTGTTAATCCCTTTTGTATCATTGTGTACA 1087
Oy      1088 AAGCTTTTCAGAAAGCTTTCTGAAATATCTTCTGTGAAAGGCAATCCAGCCACAC 1147
Db      1088 AGCGCTTTCAAAAGGCTTTCTGAAAATATTTGTATATAAAAGCAACCTTACCATGAC 1147
Oy      1148 ACAACCG 1154
Db      1148 AACACAG 1154
```

RESULT 7  
ABZ80663  
ID ABZ80663 standard; cDNA; 1173 BP.

AC ABZ80663;  
DT 13-JUN-2003 (first entry)

DE Human histamine receptor coding sequence.

human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;  
anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;  
anti-migraine; cardiac; anti-rheumatic; anti-arthritis; antipsoriatic;  
neuroprotective; inflammation; asthma; allergy; atopic dermatitis;  
myocardial infarction; migraine; chronic obstructive pulmonary disease;  
rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;  
psoriasis; receptor.

OS Homo sapiens.

FX Key Location/Qualifiers

FT CDS 1..1173  
FT /tag= a  
FT /product= "Histamine receptor"

PN US6204017-B1.

PD 20-MAR-2001.

PF 07-OCT-1999; 99US-00414010.

PR 07-OCT-1999; 99US-00414010.

PA (SCHE ) SCHERING CORP.

PI Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP,

DR WPI: 2002-442063/47.

XX P-PSDB; AB098629.

New nucleic acid encoding antigenic part of human histamine receptor,  
useful for preparing antibodies, e.g. for treating histamine related  
disorders.

PS Example 1; Col 27-28; 19pp; English.

CC This sequence represents the open reading frame for a human histamine  
CC receptor (HR) designated SP914. The sequence was isolated by searching  
CC databases with the sequence of known G-coupled protein receptor (GPCR).  
CC The gene is used for recombinant production of HR and for preparing  
CC antibodies (Ab). These Ab are used to purify HR by immunofluorescence  
CC chromatography, in immunoblotting of histamine receptor, to identify cDNA  
CC clones that express the receptor, as antagonist to block binding of  
CC histamine (for treating any histamine-associated disorder) and to  
CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR  
CC protein can be used in the treatment of e.g. inflammation, asthma,  
CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,  
CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple  
CC sclerosis, inflammatory bowel disease and psoriasis

Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 57.7%; Score 675; DB 6; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 3.5e-190;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

```
Oy      8 CAAATTAAGATGATGCGCTTACATCATTAATTTCTTGGACATTTTAATGCT 67
Db      11 CTAATGACATCATTAATTTATCCTAGACACTCGTTTACTTACATTTTATGCT 70
Oy      68 TACTAGCTATTGCTAATATGTTAGGCAATGTCGTATCTTTTATGTTAGTGA 127
Db      71 TAGTAGCTTTTGTATATATGCTAGGAATGCTTGTCTATTTTACTTTTGTGGA 130
Oy      128 GAAATCTTAGACATGAAATTAATTTTCTTAACTTGGCCATTGCACTTCTTG 187
Db      131 AAAACCTTAGACATGAAATTAATTTTCTTAACTTGGCCATTCTGCTTCTTG 190
Oy      188 TGGGTGCAATTTGCAATTCCTGTATACATACCTTCCTGCTGACTTACGAACTT 247
Db      191 TGGGTGATCTCCATTCCTTTGTATACCTTCACACCTGTTGCAATGGAAATTTG 250
Oy      248 AGCAGCTTGTATATTTTGGCTCATTTACTGACTATCTTTTATGACAGATCTGTAT 307
Db      251 AGGAATCTGTATATTTTGGCTCATTTACTGACTATCTTTTATGACAGATCTGTAT 310
Oy      308 ATATTGCTCTCATGCTACATGCTGCTACATGCTCAATGCCGTGTGTATGAG 367
Db      311 ACATTGCTCATGCTACATGCTACATGCTGCTCAATGCCGTGTGTATGAG 370
Oy      368 CTCAGCACTGTGGACCTGGAATTTGCTACTCGATGATGCTGCTTGGATATCTCT 427
Db      371 CTCACATCTAGGAGCTTGAAGATTTTACTCTGATGATGCTGCTGCTGCTCT 430
Oy      428 TCATGACAAATGGGCGATGATTCGATTTGAGACTCTTGGCAGATAGCACTAGAA 487
Db      431 TCTTAGTAATGGGCAATGATTCGATTTGAGACTCTTGGCAGATAGCACTAGAA 490
Oy      488 GTGAACCTGATTTTAAAGAGTGTACTTGTCTCTCCATCATCATTTTGAATTC 547
Db      491 GTGAACCTGATTTTAAAGAGTGTACTTGTCTCTCCATCATCATTTTGAATTC 550
Oy      548 TGATCCCATCTTGTATGTTGTTATTTAGAGGCCATTTTACTGAGGCGTGTGAAGC 607
Db      551 TGATCCCATCTTGTATGTTGTTATTTAGAGGCCATTTTACTGAGGCGTGTGAAGC 610
Oy      608 GAGAGAACTGAGAGGCTCTGAGCCACCTGTACTTCCCTGTACTCTTCCAGAGTG 667
Db      611 GATATCATCTAGTAGAGGCCAAGCCATCTCGAGCTACGTCTCTTCCAGAGTG 667
Oy      668 ACCACGACATCTCTGACAGACGAGCCCGATTTCAAGGCGACTTGCAGACGGAAG 727
Db      668 TCTGTGACATCTCATTCAGAGTGTATCTTCAAGAGATCTCTTCTGATGAGAG 727
Oy      728 AAACAACGCGCTCTTGTGCTCAGACAGTCAAGGAGAAAGAGCTCTTGTTCACA 787
Db      728 AAGTTCTGATCTTTCATTCATGAGACAGAGGAGAAAGTATGCTCATGTTTCT 787
```

QY 788 TAAGAGCTTCAAGAACAGCATATGATCGCTTCAAAATGGGCTTCTCCCACTAG 847  
 DB 788 CAGGAACCAAGATGATAGCAATACATTCCTCCAAATGGGCTTCTCCCACTAG 847  
 QY 848 ATTCCCTGGCTTTCAGCAAGGAAACATATGCAACTTTTCAGAGCCAGAAATTAGCA 907  
 DB 848 ATTCTGTAGCTTTCACCAAGGAAACATGTGTAGAGCTTTCAGAGCCAGAAATTAGCA 907  
 QY 908 AGTCATGCGCAATCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 967  
 DB 908 AGTCATGCGCAATCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 967  
 QY 968 CAGTATCTACTATTTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 1027  
 DB 968 CAGTATCTACTATTTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 1027  
 QY 1028 CATTTCCTGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCT 1087  
 DB 1028 CATTTCCTGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCT 1087  
 QY 1088 AACGTTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 1147  
 DB 1088 AACGTTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 1147  
 QY 1148 ACAACCG 1154  
 DB 1148 ACAACCG 1154  
 RESULT 8  
 ABQ78739 standard; DNA; 1173 BP.  
 XX ABQ78739;  
 DT 05-DEC-2002 (first entry)  
 XX Nucleotide sequence of human histamine receptor.  
 DE Human: histamine receptor; receptor; inflammation; asthma; allergy;  
 XX atopic dermatitis; stroke; myocardial infarction; migraine;  
 KW chronic obstructive pulmonary disease (COPD); rheumatoid arthritis;  
 KW multiple sclerosis; inflammatory bowel disease; psoriasis;  
 KW intracellular second messenger pathway; cellular growth rate;  
 KW hormone secretion; gene; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX Key CDS Location/Qualifiers  
 FT 1..1173  
 FT /tag= a  
 FT /product= "histamine receptor"  
 PN US2002098539-A1.  
 PD 25-JUL-2002.  
 XX 19-MAR-2001; 2001US-00812216.  
 PF 07-OCT-1999; 99US-00414010.  
 PR (BEHN/) BEHN J X.  
 PA (HEBR/) HEDRICK J A.  
 PA (LAZ/) LAZ T M.  
 PA (MONS/) MONSMA F J.  
 PA (MORSE/) MORSE K L.  
 PA (UMLA/) UMLAND S P.  
 PA (WANG/) WANG S.  
 PI Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;  
 PI Wang S;  
 XX

DR MPI; 2002-673827/72.  
 DR P-PSDB; AB878276.  
 XX Novel mammalian histamine receptor polypeptide useful for identifying  
 PT agonist or antagonist for treating diseases such as inflammation, asthma,  
 PT stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.  
 XX Example 1; Page 15-16; 21pp; English.  
 PS The present sequence encodes a human histamine receptor. The polypeptide  
 CC is useful for identifying an agonist or antagonist of a mammalian  
 CC histamine receptor. It is useful as an antigen to elicit the production  
 CC of antibodies. The histamine receptor polypeptide and polynucleotide are  
 CC useful in the treatment and management of diseases such as inflammation,  
 CC asthma, allergy, atopic dermatitis, stroke, myocardial infarction,  
 CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid  
 CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.  
 CC They are also useful for modulating intracellular second messenger  
 CC pathway activated through histamine receptors (cyclic-AMP, calcium,  
 CC inositol phosphate and mitogen activated protein (MAP) kinase), changes  
 CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca<sup>2+</sup>  
 CC mobilization, mitogenic effects, etc  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Query Match 57.7%; Score 675; DB 6; Length 1173;  
 Best Local Similarity 74.9%; Pred. No. 3.5e-190;  
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;  
 QY 8 CAAATACAGTACATGCGCTTACATCAATTAATTTCTTTCAGATTTTATGCTT 67  
 DB 11 CTAATAGCAATCAATTTATCACTAGACAGCTGCTTACTTTAGATTTTATGCTT 70  
 QY 68 TACTAGCTATGCTATTAATGTTAGCAATGCTGCTCATTTAGCTTTATTTGAGCA 127  
 DB 71 TAGTACCTTTTGTCTAATAGCTAGAAATGCTTGTGATTTAGCTTTTGTGTGAGCA 130  
 QY 128 GAAATCTTGACATGCAAGTAATTTACTTTTCTTAACTTGGCATTGCGAGCTTCTTG 187  
 DB 131 AATACTTGACATGCAAGTAATTTACTTTTCTTAACTTGGCATTGCGAGCTTCTTG 190  
 QY 188 TGGGTCATTTGCAATTCCTCTGTATCATCTTCTGCTGATCTTACGACTTCTGAA 247  
 DB 191 TGGGTCATTTGCAATTCCTCTGTATCATCTTCTGCTGATCTTACGACTTCTGAA 250  
 QY 248 AGCAAGCTTGTATTTTGGCTCATTCAGTATCTTTTATGTAAGCATCTGTGTATA 307  
 DB 251 AGCAAGCTTGTATTTTGGCTCATTCAGTATCTTTTATGTAAGCATCTGTGTATA 310  
 QY 308 ATATTGCTGATCAGCTAGATGCTGCTACAGTCAATTCGCGTGTATAGAG 367  
 DB 311 ACATTTGCTGATCAGCTAGATGCTGCTACAGTCAATTCGCGTGTATAGAG 370  
 QY 368 CTCAGACTTGGCAGCTGGAATTTGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 427  
 DB 371 CTCAGACTTGGCAGCTGGAATTTGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 430  
 QY 428 TCATGCAAAATGGGCGGATGATTTCTGATTTGAGCTTTGGCAATAGCATACAGAT 487  
 DB 431 TCATGCAAAATGGGCGGATGATTTCTGATTTGAGCTTTGGCAATAGCATACAGAT 490  
 QY 488 GTGAACCTGATTTTAAAAAGTGTACTTGTCTCTCCATATATATTTGGAATTC 547  
 DB 491 GTGAACCTGATTTTAAAAAGTGTACTTGTCTCTCCATATATATTTGGAATTC 550  
 QY 548 TGATCCCATCTTGTATGTTATTTGAGCGCCATATTTTATGAGAGCTGTGAGAGC 607  
 DB 551 TGATCCCATCTTGTATGTTATTTGAGCGCCATATTTTATGAGAGCTGTGAGAGC 610  
 QY 608 GAGAGAACTGAGAGGCTGCTGAGCAGCTGTAATCTCCCTGTGACTTTTCAAGCAGTG 667  
 DB 611 GTGATCATCTGATGAGGCTGAGCAGCTGTAATCTCCCTGTGACTTTTCAAGCAGTG 667

668 ACCACGACACTCTGACAGACAGACCCCGATTCAAGGGCGACTGCGACGCGAAG 727  
668 TCTGTGACACTCATTCAAGAGTAAGCTATCTTCAAGAGATCTCTTCTGCATCGACAG 727  
728 AAACAACCTGCTCTCTGTTGTTGACAGACAGTACAGGAAAGAGCACTCTCTTTTCCA 787  
728 AAGTCTGACATCTCTTCAATTCAGAGAGACAGAGGAGAAAGTGTCTCACTGTTTTCT 787  
788 TAAGACCTCAAGAAAGACAGATGTGATGCTTCCAAAATGGGCTTCTCCCACTAG 847  
788 CAGAACCAAGATGAATAGCAATACATTCCTTCCAAAATGGGCTTCTCCCACTAG 847  
848 ATTCCCTGCTCTTCAAGAAAGGAAACATATGCAATTTTCAAGACGCGAATTAAGCA 907  
848 ATTCTGTAGCTCTTCAACCAAGGAAACATGTTGAATGCTTGAAGCGCAGAGATTAGCA 907  
908 AGTCACTGGCCATCTCTTACAGAGCTTTGGCCATTTGCTGGGCTCCATTTACAGACTA 967  
908 AGTCACTGGCCATCTCTTACAGAGCTTTGGCCATTTGCTGGGCTCCATTTACAGACTA 967  
968 CAGTATCTACTCATTCTTCTGAAAGGAAAGCACTTGACATCAACCTGTAACATCTG 1027  
968 CATTGTCTCTTCAATTTATCTCTGACGAAAGCTCTAAATCACTTGTGATAGAAATTG 1027  
1028 CCTTTGCTCAGAGTGTCAATCTCTTTGTAATCCTTTTGTATTCATTTGTGTACA 1087  
1028 CATTGTGCTTCAAGTGTCAATCTCTTTGTAATCCTTTTGTATTCATTTGTGTACA 1087  
1088 AACGTTTCAAGAGCTTCTGAAATATCTTCTGTGAAAGGCAATCAGCCGACAC 1147  
1088 ACGGCTTCAAGAGCTTCTGAAATATCTTGTATTAATAAAGCAACCTTACCATCAGC 1147  
1148 ACAACCG 1154  
1148 AACACAG 1154

RESULT 9  
AA170980  
ID AA170980 standard; cDNA; 1173 BP.  
XX  
AC AA170980;  
XX  
18-MAR-2002 (first entry)  
XX  
DE Human histamine H4 receptor cDNA.  
XX  
Histamine H4 receptor; human; antihistaminic; antiallergenic;  
KM antinflammatory; cardiac; circulatory; antidiabetic; laxative;  
KM diagnosis; gene therapy; ss.  
XX  
Homo sapiens.  
OS  
XX  
PN MO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;  
XX  
DR MPI; 2002-114339/15.  
XX  
DR P-PSDB; AAM50564.  
XX  
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
XX the proteins, useful in gene therapy for treating diseases where it is  
XX beneficial to elevate mammalian histamine H4 receptor activity.  
PS Claim 4; Fig 1; 92pp; English.

XX  
CC The present sequence is that of cDNA clone pH4R encoding a human  
CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone  
CC marrow cDNA library. The invention provides mammalian (human, mouse, rat  
CC and guinea pig) histamine H4 receptor nucleic acid molecules (see  
CC AA170980-83) and polypeptides (see AAM50564-67). The nucleic acids have  
CC been expressed in recombinant host cells that produce active recombinant  
CC protein. The pharmacology of known histamine ligands is demonstrated.  
CC Mammalian histamine H4 receptor may be used in gene therapy for the  
CC treatment of diseases where it is beneficial to elevate mammalian  
CC histamine H4 receptor activity. Recombinant protein is useful for  
CC identifying modulators of the human histamine H4 receptor. Such  
CC modulators may be useful for diagnosing, treating or preventing asthma,  
CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-  
CC insulin dependent diabetes mellitus, hyperglycemia, constipation,  
CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity

SQ  
Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
Query Match 57.7%; Score 675; DB 6; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 3.5e-190;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;  
8 CAAATPACAGTACAAATCCGCTTAACATCAATTAATTTCTTGAACATTTTAAATGCTT 67  
11 CTAATAGACACATCAATTTATCATAACACACGCTGTATTAATTTTATGTCCT 70  
68 TACTAGCTATTGCTTAATGTTAGGCAATGCTGCTATTTTACCTTTATTTAGGACA 127  
71 TAGTAGCTTTGCTTAATGCTGAGAAATGCTTGTATTTAGCTTTTGTGTGAGACA 130  
128 GAAATCTTAGACATGAAATATTAATTTTCTTAATCTTGGCAATGCGACTTCTTGG 187  
131 AAAACCTTAGACATGAAATGCTTATTTTCTTAATCTTGGCAATCTGACTTCTTGG 190  
188 TGGGTGCAATTGCAATTTCTCTGTACATACCTTCTCGTGACTTAAGTACTTCTGAA 247  
191 TGGGTGCAATCTCCTTCTTGTATCTTCTTGTATCTTCTGCAACGCTGTGCAATGGAATTTGGAA 250  
248 AGCAAGCTTGTGATTTTGGCTCATTAAGTATCTTTATTTATGACAGCATGCTGTATA 307  
251 AGCAATCTGCTGATTTTGGCTCATTAAGTATCTTTATTTATGACAGCATGCTGTATA 310  
308 AATATGCTCTCATGACATGACATGCTGCTACAGTCAATGCTGCTGTATGATAGAG 367  
311 AATATGCTCTCATGACATGACATGCTGCTACAGTCAATGCTGCTGTATGATAGAG 370  
368 CTCAGACCTTGGCACTCGGAAATTTGCTACATGATGCTGCTGTTTGAATATCTCCT 427  
371 CTCAGACATGCTGGGCTTGGAAATGCTGCTGATGCTGCTGCTGCTGCTGCTGCT 430  
428 TCATGACAAATGGGCGATGATTTGATTTAGACTCTGGGAGATAGACATACAGAT 487  
431 TCTTAGTAATGGGCAATGATTTCTAGTTTCAAGATCTTGGAGATGAAGTATGAT 490  
488 GTGAACCTGATTTTAAAGGATGCTTCTCTCCATCATCATTTATTTGAATTC 547  
491 GTGAACCTGATTTTAAAGGATGCTTCTCTCCATCATCATTTATTTGAATTC 550  
548 TGATCCCATCTTGTAGTTGCTTATTTTCAAGGCTGCTTATTTACATGACCTGTGAAC 607  
551 TGATCCCATCTTGTAGTTGCTTATTTTCAAGGCTGCTTATTTATTTGAACCTGTGAAC 610  
608 GAGAGAACTGACAGGCTGCTGACGACCTGTAATCCCTCTGACTCTTCCAGAGTG 667  
611 GTGATCATCTCAATGCTGCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667  
668 ACCACGACACTCTGACAGACAGACCCCGATTCAAGGGCGACTGCGACGCGAAG 727  
668 TCTGTGACACTCATTCAAGAGTAAGCTATCTTCAAGAGATCTCTTCTGCATCGACAG 727  
728 AAACAACCTGCTCTCTGTTGTTGACAGACAGTACAGGAAAGAGCACTCTCTTTTCCA 787

Db 728 AGTTCCTGCATCCTTTTCATTCAGAGAGACAGAGAAAGTAGTTCATGTTTCT 787  
 Qy 788 TAGAGCCTACAGAACAGCAATGTATGCTCCAAAAGGGCTTCCTCCACTCAG 847  
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 Qy 908 AGTCACTGGCCATCTCTTTCAGAGCTTTGGCCATTTGCTGCTCCATATTCATGACTA 967  
 Db 908 AGTCACTGGCCATCTCTTTCAGAGCTTTGGCCATTTGCTGCTCCATATTTCTGTTCA 967  
 Qy 968 CAGTTATCTACTATTTTTCCTGAAAGAACTGACTAATGACCTGTACCATACG 1027  
 Db 968 CAGTTATCTCTTATTTTATTTCTGCAAGCAAGCTCTAATAGTTGTATAGAAATG 1027  
 Qy 1028 CTTTTCAGCTCAGTGGTCAATTCCTTTGTATCTCTTTGTATCCATGTGTACA 1087  
 Db 1028 CATTTCGCTTCAGTGGTCAATTCCTTTGTATCTCTTTGTATCCATGTGTACA 1087  
 Qy 1088 AACGTTTTCAGAAAGCTTTCTGAAATATCTCTGTGAGAGCAATCCACCCAC 1147  
 Db 1088 AGGCTTTTCAAAAGCTTTCTGAAATATTTGTATTTAAAGCAACCTCTACCATCAG 1147  
 Qy 1148 ACAACCG 1154  
 Db 1148 AACACAG 1154  
 RESULT 10  
 AA167750  
 ID AA167750 standard; cDNA; 1173 BP.  
 AC AA167750;  
 XX  
 DT 27-FEB-2002 (first entry)  
 XX  
 DE Human histamine H4 receptor protein encoding cDNA.  
 XX  
 KM Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;  
 KM antidiabetic; antiallergic; neuroprotective; antidiabetic; human;  
 KM cerebroprotective; cAMP modulator; gene therapy; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..1173  
 FT /tag= a  
 FT /product= "histamine H4 receptor"  
 FT  
 XX  
 PN W0200185786-A2.  
 PD 15-NOV-2001.  
 XX  
 PF 04-MAY-2001; 2001MO-US014527.  
 XX  
 PR 05-MAY-2000; 2000US-0202151P.  
 PR 23-AUG-2000; 2000US-0227567P.  
 PR 13-NOV-2000; 2000US-0247855P.  
 XX  
 PA (AMHP ) AMERICAN HOME PROD CORP.  
 PI Jones PG, Blatcher M, Wu S, Pausch MH;  
 XX WPI; 2002-049442/06.  
 DR P-PSDB; AAG66023.  
 XX  
 PT New histamine receptor, termed H4 useful for detecting H4 (ant)agonists  
 PT for treating transplanted organ rejection, asthma, allergy, multiple  
 PT sclerosis and rheumatoid arthritis.  
 XX

PS Claim 13; Fig 1; 66pp; English.  
 XX  
 CC The invention provides an isolated histamine receptor, H4, which binds  
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4  
 CC receptor can be expressed by standard recombinant methodology. Cells  
 CC expressing H4 receptor protein at a detectable level can suppress cyclic  
 CC adenosine monophosphate (cAMP) formation when contacted with the H4  
 CC receptor agonist. The H4 receptor and antibodies are used for identifying  
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful  
 CC for treating transplanted organ rejection, asthma, allergies and  
 CC autoimmune pathologies such as multiple sclerosis, type I diabetes,  
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor  
 CC protein and nucleic acids are useful targets to identify drugs that are  
 CC effective in treating disorders associated with histamine-regulated  
 CC processes. Identification and isolation of H4 receptor provides for  
 CC development of screening of molecules that interact with H4 receptors.  
 CC Genetic variants of H4 can be used to diagnose an H4 associated disease  
 CC as described above. The H4 receptor polynucleotide is useful to treat or  
 CC prevent a disorder associated with the function of H4 in peripheral blood  
 CC leukocytes. The present sequence represents a cDNA encoding the human  
 CC histamine H4 receptor protein  
 XX  
 SQ Sequence 1173 BP; 296 A; 245 C; 231 G; 401 T; 0 U; 0 Other;  
 Query Match 57.7%; Score 675; DB 6; Length 1173;  
 Best Local Similarity 74.9%; Pred. No. 3,5e-190;  
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;  
 Qy 8 CAAATTAACAGTACATGCGCTTAACATCAATTAATAATTTCTTGTACATTTTAATGCTT 67  
 Db 11 CTATATGACAAATCAATTAATTAATCACTAAGCACTGCTTACTTATGATTTTATGTCTT 70  
 Qy 68 TACTACTATGCTATTAATATTAGCAATGCTGCTATTTTATGCTTTTATTTATGAGCA 127  
 Db 71 TAGTACCTTTTGTATTAATGCTAAGAAATGCTTGTATTTTATTTAGCTTTTGTGAGCA 130  
 Qy 128 GAAATCTTACAGATCAAGATTAATTAATTTTCTTAACTTGGCCATTTGAGACATTTCTTG 187  
 Db 131 AAAACCTTACAGATCAAGATTAATTTTCTTAACTTGGCCATTTGAGACATTTCTTG 190  
 Qy 188 TGGTGCAATTTGCAATTTCTGTATACATCTTCTGCTGACTTACATGACATTTCTGAA 247  
 Db 191 TGGTGCAATTTGCAATTTCTGTATACATCTTCTGCTGACTTACATGACATTTCTGAA 250  
 Qy 248 AGCAAGCTGTGATTTTGGCTATTAATGACATCTTCTTATTAATGACATCTGATATA 307  
 Db 251 AGCAAGCTGTGATTTTGGCTATTAATGACATCTTCTTATTAATGACATCTGATATA 310  
 Qy 308 ATATGCTCATCACTAGATGATGCTTACAGTCAAGTCAATTTGCGTGTATATAGAG 367  
 Db 311 ACATGCTCATCACTAGATGATGCTTACAGTCAAGTCAATTTGCGTGTATATAGAG 370  
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 Db 371 CTCAGCACTCTGGACCTGGAATAATTTGCTAATGATGCTGCTGATTTGATTTCTCTT 430  
 Qy 428 TCATGCAAAATGGGCGGATGATTTGATTTGACATCTTTGGAGATAGACATACGAAT 487  
 Db 431 TCTTAGTGAATGGGCGGATGATTTGATTTGACATCTTTGGAGATAGACATACGAAT 490  
 Qy 488 GTGAACCTGATTTTAAAGATGATGCTTCTGCTTACATCATATTATTTGGAATTC 547  
 Db 491 GTGAACCTGATTTTAAAGATGATGCTTCTGCTTACATCATATTATTTGGAATTC 550  
 Qy 548 TGAATCCCATCTTGTATGCTTATTTTCAAGCGCCATATTTTACGAGCGTGTGAAGC 607  
 Db 551 TGAATCCCATCTTGTATGCTTATTTTCAAGCGCCATATTTTACGAGCGTGTGAAGC 610  
 Qy 608 GAGAGAAATGAGACAGTGTCTGACCACTGTATCTCCCTGTACTCTTTCAGAGAG 667  
 Db 611 GTATATATCTCAGTAGTGTCCAAAGCAATCTGAGATGCTGTGTCTTCCACAA--- 667  
 Qy 668 ACCACGACACTCTGACAGACAGACCCGATTCAGAGCGACTGTGCCAGACGAAAG 727



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Db 491 GTGAACCTGATTTTTCGGAAATGATACCTTCGCATCATCATATCTTGGAAATTCG 550
Qy 548 TGAATCCCATCTTTGTAATGTTGCTTATTTGAGCCCATATTTAGAGCTTGGAAGC 607
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Qy 608 GAGAGAACTGACAGAGTGCCTCAGCAGCCCTGTAACCTCCCTGTAACCTTCCAGCAGTG 667
Db 611 GTGATCATCTCAATAGTGTGCAAAAGCCATCTGGAATGAGTGTCTTCCAAACA--- 667
Qy 668 ACCAGCAGACCTCTGAGAGAGAGCCCGATTTCAAGGGGAGTCTGCGCAGACGGAAG 727
Db 668 TCTGTGAGACCTCATTCAGAGAGTGAATCTTCAAGAGAGATCTCTTTCGATCGACAG 727
Qy 728 AAACAACTGCTCTCTTGGTTCAGACAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 787
Db 728 AAGTTCCTGATCTTTCATTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
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Db 848 ATTCCTGCTCTTTCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
Qy 908 AGTCACTGCGCATCTTTCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
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Qy 968 CAGTTATCTACTATTTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
Db 968 CAGTTATCTACTATTTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
Qy 1028 CTTTTCCTGCTCAGTGTGATCAATTCCTTGTATTCCTTGTATTCATTCATTCATTC 1087
Db 1028 CTTTTCCTGCTCAGTGTGATCAATTCCTTGTATTCCTTGTATTCATTCATTCATTC 1087
Qy 1088 AAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1147
Db 1088 AAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1147
Qy 1148 ACAACCG 1154
Db 1148 AACACAG 1154

RESULT 12
ADG98759
ID ADG98759 standard; cDNA; 1173 BP.
XX
AC ADG98759;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human orphan GPCR cDNA, RUP7.
XX
KW Human; G protein-coupled receptor; GPCR; research tool; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1173
FT /tag= a
FT /product= "Human GPCR protein"
XX
PN US2003148450-A1.
XX
PD 07-AUG-2003.
XX
PF 17-OCT-2002; 2002US-00272983.
XX

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PR 20-NOV-1998; 98US-0109213P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123949P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0137217P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-0141448P.
PR 28-SEP-1999; 99US-0156333P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156634P.
PR 12-OCT-1999; 99US-00417044.

XX
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAN/) LIAN C W.
PA (LINI/) LIN I.
XX
PI Chen R, Dang HT, Lian CW, Lin I;
XX
DR WPI; 2003-897571/82.
XX
DR P-PSDB; ADG98760.
XX
PT New cDNA encoding a human G protein coupled receptor, useful for making a
PT probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR
PT identification of the expression of the receptor in tissue samples.
XX
PS Claim 25; SEQ ID NO 13; 52bp; English.
XX
CC The present invention provides novel human G protein-coupled receptor
CC (GPCR) proteins and their encoding nucleic acids. The invention is useful
CC for making a probe for dot-blot analysis and for RT-PCR identification of
CC the expression of the receptor in tissue samples. The invention is also
CC useful for identifying candidate compounds as inverse agonists, agonists
CC or partial agonists and as research tools in determining the location of
CC the receptors within the body. The present sequence is human orphan G
CC protein-coupled receptor cDNA.
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 57.7%; Score 675; DB 10; Length 1173;
Best Local Similarity 74.9%; Pred. No. 3, 5e-190;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAATATACAGTACATCGCCTTAACATCAATTAATTTCTTGAATTTTATGCTT 67
Db 11 CTAAATGACACATCAATTTATCTACTAGACATCGCTTACTTATGATTTTATGCTT 70
Qy 68 TACTAGCTATGCTATATATGTTAGGCAATGTCGTGTCATTTTATGTTAGTGA 127
Db 71 TACTAGCTTGTCTATATATGCTAGGAATGCTTGTGTCATTTTATGTTAGTGA 130
Qy 128 GAAATCTTACATTCAGAGATTAATTTTCTTAACTTGGCATTTGAGAGATTTCTT 187
Db 131 AAACCTTACATTCAGAGATTAATTTTCTTAACTTGGCATTTGAGAGATTTCTT 190
Qy 188 TGGGTCAATTTGCAATTTCTCTGATACATCTTCTGATGATTTCTGATTTCTGAA 247
Db 191 TGGGTGATGATCTCATTTCTTGTATACCTCTCACAGCTGTTGCAATGGAATTTTGA 250
Qy 248 AGCAAGCTGTGATTTTGGCTGATTAATGATCTTTTATGATGATGATGATGATG 307
Db 251 AGGAAATCTGTGATTTTGGCTGATTAATGATCTTTTATGATGATGATGATGATG 310
Qy 308 ATATTTGCTCAGTACAGATGATGATGATGATGATGATGATGATGATGATGATG 367
Db 311 ACATTTGCTCAGTACAGATGATGATGATGATGATGATGATGATGATGATGATG 370
Qy 368 CTCAGCATCTGACACTGGAATTAATTTACTAGATGATGATGATGATGATGATG 427

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Db	371	CTCAACATACCTGGGGCTCTTGAAGATTGTTACTCTGATGTGCGCTTGTTGGTCTGGCTT	430
Qy	428	TCATGACAAATGGGGCGATGATTCCTGATTTGAGACTCTTGGCAGAAATAGCACTACAGAAAT	487
Db	431	TCTTAGTGAATGGGGCAATGATTCCTAGTTTCAAGAGTCTTTGGAAGGATGAAGTAGTGAAT	490
Qy	488	GTGAACCTGGAATTTTAAAAAAGTGTACTTTGCTCTCCCTACATCATTTATTGAAATCC	547
Db	491	GTGAACCTGGAAATTTTTTTCGGAATGTGTACATCTCTTGCCATCAATCATTTCTGGAAATTCG	550
Qy	548	TGATCCCATCTGTGTAGTGTGCTAATTCAGGGCCATATTATCTGGAGCCGTGGGAAGC	607
Db	551	TGATCCCATCTATCTTAGTCGTTCGTTATTTTCAACATGAATATTTATTTGAGCCGTGGGAAGC	610
Qy	608	GAGAGAAACTGAGCAGGTGCTCAGCCACCCGTGTACTCCCTCTGACTCTTCCAGCAGTGTG	667
Db	611	GTGATTCATCTCAGTAGTGGTCCAAAGCCATCTCGACTCATCTGTCTCTTCCAAACA---	667
Qy	668	ACCAAGCACTCTCTGCAAGACAGACCCCGATTCAAGGGCCGACTCTGTCAGCAACGGAAG	727
Db	668	TCTGTGACACTCATTTCCAGAGTAGACTATCTTCAAGAGAGATCTCTTCTGCATGACAG	727
Qy	728	AAACAATGCTCTCTTGTGGTTCAAGCAAGTCAAGGAAAGACAGTCTTGTGTTTCCA	787
Db	728	AAATTCCTGCAATCTTTTCATTTCAGAGACAGAGGAGAAAGATGTCTCATGTGTTTCTT	787
Qy	788	TAAAGCCTTACAAAGAACAGAAATGATGATCGCTTCCAAATAGGGCTTCTCTCCCACTGAG	847
Db	788	CMAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATAGGGTCTCTTCTCCCAATAG	847
Qy	848	ATTCCTGAGCTCTTCAGCAAGAAAGGAACATATCGAACTTTTCAGAGCCAGAAATTAGCCA	907
Db	848	ATTCTGTATGCTCTTCAACCAAGGGGAACATGTGAATCTGTAAGCCAGAGATTAGCCA	907
Qy	908	AGTCACTGGCCAACTCTTAGGGGTTTGTGCTGTGCTGGGCTCCAAATATCTCTGTCA	967
Db	908	AGTCACTGGCCAACTCTTAGGGGTTTGTGCTGTGCTGGGCTCCAAATATCTCTGTCA	967
Qy	968	CAGTTATCTACATTTTTTCTCTGAAAGAACTTGAATCAACCTGATACCATCTG	1027
Db	968	CAATTTGCTCTTCAATTTTATTTCTCAGCAACAGGTCTCAATATCACTTTGGTATGAATTG	1027
Qy	1028	CCTTTGGCTCCAGTGTTCATATTCCTTGTTAATCCCTTTTGTATCCATTTGTGTCA	1087
Db	1028	CATTTTGGCTTCAGTGTTCATATTCCTTGTTCATATTCCTTTTGTATCCATTTGTGTCA	1087
Qy	1088	AACGTTTTCAGAAAGGCTTCTCTGAATAATCTTCTGTGAAGAGGCAATCCACGCCACAC	1147
Db	1088	AGCGCTTTCAGAAAGGCTTCTCTGAATAATTTTGTATTAATAAAGCAACCTCATCATCAC	1147
Qy	1148	ACAACCG 1154	
Db	1148	AACATAG 1154	

RESULT 13  
ABS57063  
ID ABS57063 standard; cDNA; 1173 BP.

XX  
AC  
ABS57063;

XX 28-JAN-2003 (first entry)  
DT

AA Human cDNA encoding G-protein coupled receptor AXOR35.  
DE

Human; ss; gene; G-protein coupled receptor; AXOR35; Lymphocyte;

KW macrophage; eosinophil; neutrophil; infection; transplant rejection;  
KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease

KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;  
KX celiac disease; irritabile bowel syndrome; vomiting; inflammation;

KM myocardial infarction; hypertension; pulmonary disorder;  
myocardial infarction; hypertension; pulmonary disorder;  
KM psoriasis; urological disease; urinary retention; cardiovascular disease;

KW chronic obstructive pulmonary disease; cough; renal disease;  
KW renal ischaemia; arteriosclerosis, atherosclerosis; psychosis;  
KW neurological disorder; migraine; anorexia; anxiety; schizophrenia;  
KW dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;  
KW graft versus host disease; osteoporosis.

**Homo sapiens.**

Key	Location/Qualifiers
25	
FH	
25	

24 000  
FT / \*tag= a

XX  
XX

XXXXXXXXXXXX

9	XX
8	
7	
6	
5	
4	
3	
2	
1	

22	20	2001	00010411
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22	NOV 1960	OCTO 00431000
XX		

PR	03-FEB-2000; 2000US-00497790
DE	28 OCT 2000 0000UTC 0000000000

XX  
XX  
XX

(CONTINUED) SWITZERLAND RECEIVING COUNTRIES

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Aubart KM, Bergsma DJ, Fitzgerald L, Graybill TL, Li X; Michalowski D, Merson D, Zhu Y

XX  
DB  
WBT, 2003-074000/07

DR P-PSDB; ABG71960.

**PT** Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infectious disorders autoimmune disorders

PT urological diseases, cardiovascular diseases and cancer.

PS Claim 2; Page 21-22; 24pp; English  
xy

CC The invention relates to an isolated G-protein coupled receptor

CC polynucleotide (and its homologues, variants, complements and RNA equivalents) also included are an anti-AV025 antibody, an AV025

CC expression vector, producing a recombinant host cell by introducing the CC vector into a cell such that the host cell produces AY035, a membrane of

CC the host cell expressing AXOR35, identifying/screening for agonists or antagonists of AXOR35 and inhibiting or promoting the function of

CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue, CC by administering to the patient AY0P25 agonists or antagonists. The

agonist or antagonist identified is useful for treating a disease such as asthma or for inhibiting or promoting the function of lymphocytes

CC macrophages, eosinophils, or neutrophils in diseased tissue such as an asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays

CC for identifying compounds that are agonists or antagonists of AXOR35, as  
CC vaccines, or for treating infections (bacterial, fungal, protozoan or

CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),

CC Irritable bowel syndrome, vomiting, inflammation (such as atopic dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis, CC

CC psoriasis), urological diseases (such as urinary retention),  
CC cardiovascular diseases (such as myocardial infarction), hypertension.

CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary disease), cough, renal diseases (such as renal ischaemia).

CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders  
CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such

CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft versus host disease and osteoporosis. The present sequence is the cDNA

CC encoding AXOR35  
XX

Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match	57.7%	Score 675;	DB 10;	Length 1173;
Best Local Similarity	74.9%	Pred NO 3	5e-190.	

Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1,

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QY 8 CAATTAACAGTACGACCTTAACATCAATTAATAATTTCTTGACATTTTAAATGCTT
DB 11 CTATATGCAACAATTAATTAATTAACAGACCTGCTGTACTTAAAGATTTTATATGCTT
QY 68 TACTAGCTATTTGCTAATTAATTAATTAAGCAATGCTGCTGCTATTTTAAATTTATGAGCA
DB 71 TAGTACTTTTGTCTAATAATTAATTAAGCAATGCTGCTGCTATTTTAAATTTATGAGCA
QY 128 GAAATCTTGAACATTAATTAATTAATTAATTTCTTAACTTTGAGCACTTCTTCTT
DB 131 AAAACCTTGAACATTAATTAATTAATTAATTTCTTAACTTTGAGCACTTCTTCTT
QY 188 TGGGTCAATTTGAAATTTCTCTGTAACATTAATTTCTTCTGTAACATTTCTGTAACATTTCTG
DB 191 TGGGTGATTTCTCAATTTCTTCTGTAACATTTCTTCTGTAACATTTCTGTAACATTTCTG
QY 248 AGCAAGCTTGTATTTTGTGCTATTAATTAATTAATTTCTTAACTTTTAAATTTATGAGCA
DB 251 AGCAAGCTTGTATTTTGTGCTATTAATTAATTAATTTCTTAACTTTTAAATTTATGAGCA
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DB 311 ACATTTGCTTCTGATTAATTAATTAATTAATTTCTTAACTTTTAAATTTATGAGCA
QY 368 CTCAGCACTTGTGCACTTGTGCACTTGTGCACTTGTGCACTTGTGCACTTGTGCACTTGTG
DB 371 CTCAGCACTTGTGCACTTGTGCACTTGTGCACTTGTGCACTTGTGCACTTGTGCACTTGTG
QY 428 TCATGACAAATGAGCGAGATTTCTGATTTTCAAGCTTTTCAAGCTTTTCAAGCTTTTCAAG
DB 431 TCTTAGGAAATGAGCGAGATTTCTGATTTTCAAGCTTTTCAAGCTTTTCAAGCTTTTCAAG
QY 488 GTAACTTGTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT
DB 491 GTAACTTGTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT
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DB 611 GATGATATCTGATTAATTAATTAATTAATTTCTTAACTTTTAAATTTATGAGCA
QY 668 ACCAGGACATCTTGTGACAGAGATTTCTGATTTTCAAGCTTTTCAAGCTTTTCAAG
DB 668 TCTGTGACATCTTGTGACAGAGATTTCTGATTTTCAAGCTTTTCAAGCTTTTCAAG
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DB 728 AAACAACTGCTCTTGTGACAGAGATTTCTGATTTTCAAGCTTTTCAAGCTTTTCAAG
QY 788 TAAAGCTTGAACATTAATTAATTAATTTCTTAACTTTTAAATTTATGAGCA
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DB 908 AGTCACTGAGCATTTCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT
QY 968 CAGTTATCTGATTTTCTGAGCAAGATTTCTGATTTTCAAGCTTTTCAAGCTTTTCAAG
DB 968 CAGTTATCTGATTTTCTGAGCAAGATTTCTGATTTTCAAGCTTTTCAAGCTTTTCAAG
QY 1028 CATTGCTTCTGATTTTCTGAGCAAGATTTCTGATTTTCAAGCTTTTCAAGCTTTTCAAG
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DB 1088 AGCGTTTTCAGAGGCTTTCTGAGAAATTAATTTCTGAGAGGCAATCCAGCCAC 1147
QY 1148 ACAACG 1154
DB 1148 AACACAG 1154

RESULT 14
ADJ26922 standard; cDNA; 1173 BP.
ID ADJ26922;
AC ADJ26922;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endogenous orphan G-protein coupled receptor RUP7 cDNA.
XX
KW Human; G protein-coupled receptor; GPCR; dot-blot analysis;
KW pharmaceutical agent; gene; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1173
FT /tag= a
FT /product= "Human endogenous orphan GPCR protein"
XX
PN US2003175891-A1.
PD 18-SEP-2003.
XX
PF 21-MAR-2003; 2003US-00393807.
XX
PR 20-NOV-1998; 98US-0109213P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123949P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-014148P.
PR 28-SEP-1999; 99US-0156333P.
PR 28-SEP-1999; 99US-0156555P.
PR 28-SEP-1999; 99US-0156634P.
PR 28-SEP-1999; 99US-0156653P.
PR 29-SEP-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00417044.
PR 17-OCT-2002; 2002US-00272983.
XX
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAN/) LIAN C W.
PA (LIN/) LIN I.
PI Chen R, Dang HT, Lian CW, Lin I;
XX
DR WPI; 2003-898539/82.
DR P-PSDB; ADJ26923.
XX
PT New human G protein-coupled receptor and its coding cDNA, useful for
PT disease or disorder identification and/or selection, for screening of
PT candidate compounds useful as pharmaceutical agents, and in research
PT applications.
```

XX Claim 25; SEQ ID NO 13; 53bp; English.

CC The present invention relates to human endogenous orphan G protein-  
CC coupled receptor (GPCR) proteins and polynucleotides encoding such  
CC proteins. The cDNA sequence of the human G protein-coupled receptor  
CC (GPCR) is useful in making a probe for dot-blot analysis against tissue-  
CC mRNA and/or for RT-PCR identification of the expression of the receptor  
CC in tissue samples. GPCR sequences of the invention may be used in  
CC disease/disorder identification and/or selection, in screening of  
CC candidate compounds for use as pharmaceutical agents and in research  
CC settings. The present sequence is human endogenous orphan GPCR cDNA.

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 57.7%; Score 675; DB 11; Length 1173;

Beet Local Similarity 74.9%; Pred No. 3.5e-190;

Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

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QY      8 CAAATTAACGATCAATCCGCTTAACATCAATTAATTAATTTCTTGAACATTTTATGTCCT 67
DB      11 CTAAATAGCAATCAATTTATCATCAAGCACTCGTGTACTTTAGACATTTTATGTCCT 70
QY      68 TACTAGCTATTGCTATTAATGTTAGCAATGCTGTCATTTTACTTTTATTTAGTGACA 127
DB      71 TAGTAGCTTTTCTATTAATGCTAGAAAGCTTTGGTCAATTTAGCTTTTGTGTGACA 130
QY      128 GAAATCTTACATGAGATGAATTAATTAATTTCTTTTAACTTGGGCAATGCGACTTCTTG 187
DB      131 AAAACCTTACATGAGATGAATTAATTTCTTTTAACTTGGGCAATGCGACTTCTTG 190
QY      188 TGGGTGACATTCGCTCTGTATACATCTTCTCGCTGACTTACTGAGCTTCGAA 247
DB      191 TGGGTGATCTTCATCTCTTGTATACATCTTCTCGCTGACTTACTGAGCTTCGAA 250
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## RESULT 15

ADG86374 ID ADG86374 standard; cDNA, 1173 BP.

ADG86374;

11-MAR-2004 (first entry)

Human endogenous orphan GPCR hRUP7 cDNA.

Human; ss; gene; endogenous orphan GPCR; G protein-coupled receptor;

transmembrane domain 6.

Homo sapiens.

US2003229216-A1.

11-DEC-2003.

16-APR-2003; 2003US-00417820.

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XX      13-OCT-1998; 98US-00170496.
PR      12-NOV-1998; 98US-0108029P.
PR      20-NOV-1998; 98US-0109213P.
PR      27-NOV-1998; 98US-0110060P.
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PR 01-OCT-1999; 99US-0157280P.  
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 PR 01-OCT-1999; 99US-0157284P.  
 PR 12-OCT-1999; 99US-00416760.  
 XX  
 PA (CHEN/) CHEN R.  
 PA (LIAM/) LIAM C W.  
 PA (LOWI/) LOWITZ K.  
 PA (CHAL/) CHALMERS D T.  
 PA (BEHA/) BEHAN D P.  
 PI Chen R, Liam CW, Lowitz K, Chalmers DT, Behan DP;  
 XX WPI, 2004-052038/05.  
 DR P-PSDB; ADG86375.  
 XX  
 PT New cDNA encoding a non-endogenous, constitutively activated version of a  
 PT human G protein-coupled receptor, useful for identifying receptor.  
 PT Inverse or partial agonists having potential applicability as therapeutic  
 PT agents.  
 XX  
 PS Example 1; SEQ ID NO 13; 110pp; English.  
 XX  
 CC The invention relates to a cDNA encoding a non-endogenous, constitutively  
 CC activated version of a human G protein-coupled receptor comprising hARE-  
 CC 3(F313K), hARE-4(V233K), hARE-5(A240K), hGPCR14(L257K), hGPCR27(C283K),  
 CC hARE-1(E232K), hARE-2(G285K), hEPRI (L239K), hG2A(K232A), hRUP3(L224K),  
 CC hRUP5(A236K), hRUP6(N267K), hRUP7(A302K), hCHN4(V234K), hCHN5(S224K),  
 CC hCHN6(L252K), hCHN8(N235K) or h9(F236K). Also included are  
 CC a non-endogenous version of a human G protein-coupled receptor encoded by  
 CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell  
 CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively  
 CC activated version of a human G protein-coupled A71 receptor comprising  
 CC the angiotensin II type 1 receptor hAT1(F239K), hAT1(N11A),  
 CC hAT1(AT2451C3, a domain swap mutant) or hAT1(A243+). The mutation is of  
 CC an amino acid 16 residues from the proline in transmembrane domain 6 and  
 CC is usually to a lysine. The cDNA is useful for identifying candidate  
 CC compounds as receptor agonists, inverse agonists or partial agonists  
 CC having potential applicability as therapeutic agents. The present  
 CC sequence is a cDNA (or fragment) for a wild-type human GPCR.  
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 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Query Match 57.7%; Score 675; DB 12; Length 1173;  
 Best Local Similarity 74.9%; Pred. No. 3.5e-190;  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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9761.031 Million cell updates/sec

Title: US-10-626-398-7

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Searched: 7297361 seqs, 3241162794 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	675	57.7	1173	9	US-09-910-411-1
6	675	57.7	1173	10	US-09-875-076-13
7	675	57.7	1173	10	US-09-876-252-13

8	675	57.7	1173	13	US-10-052-193-1	Sequence 1, Appl1
9	675	57.7	1173	15	US-10-272-983-13	Sequence 13, Appl1
10	675	57.7	1173	15	US-10-354-769-1	Sequence 1, Appl1
11	675	57.7	1173	16	US-10-393-807-13	Sequence 13, Appl1
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13	675	57.7	1173	18	US-10-349-253A-1	Sequence 1, Appl1
14	675	57.7	1173	19	US-10-723-955-13	Sequence 13, Appl1
15	675	57.7	1173	19	US-10-782-596-13	Sequence 13, Appl1
16	675	57.7	1173	19	US-10-737-619-1	Sequence 1, Appl1
17	675	57.7	1173	21	US-10-626-445-1	Sequence 1, Appl1
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23	675	57.7	1300	19	US-10-696-673-1	Sequence 1, Appl1
24	675	57.7	3689	21	US-10-225-567A-628	Sequence 628, App
25	675	57.7	3689	21	US-10-684-206-19	Sequence 19, Appl1
26	671.8	57.4	1173	15	US-10-290-078-26	Sequence 26, Appl1
27	671.8	57.4	1265	15	US-10-290-078-25	Sequence 25, Appl1
28	616.8	52.7	1176	20	US-10-626-445-6	Sequence 6, Appl1
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33	613	52.4	1176	21	US-10-626-398-5	Sequence 5, Appl1
34	270	23.1	1326	19	US-10-398-036-19	Sequence 19, Appl1
35	155.4	13.3	1223	19	US-10-283-975A-637	Sequence 637, App
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#### ALIGNMENTS

RESULT 1  
US-10-626-445-7  
; Sequence 7, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PBD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; PRIOR FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 1170  
; TYPE: DNA  
; ORGANISM: Cavia porcellus  
US-10-626-445-7

Query Match 100.0%; Score 1170; DB 20; Length 1170;  
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RESULT 2  
US-10-626-126-7  
Sequence 7, Application US/10626126  
Publication No. US20050074770A1  
GENERAL INFORMATION:  
APPLICANT: Lovenberg, Timothy  
APPLICANT: Liu, Changlu  
TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
FILE REFERENCE: PRD-0033  
CURRENT APPLICATION NUMBER: US/10/626,126  
CURRENT FILING DATE: 2003-07-23  
PRIOR APPLICATION NUMBER: 09/790,849  
PRIOR FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 60/208,260  
PRIOR FILING DATE: 2000-05-31  
NUMBER OF SEQ ID NOS: 27  
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SEQ ID NO 7  
LENGTH: 1170  
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US-10-626-126-7  
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1 ATGTTGGCAATTAACAGTACAAATGCGCTTAACATCAATTAATTTCTTGACATTTT 60  
1 ATGTTGGCAATTAACAGTACAAATGCGCTTAACATCAATTAATTTCTTGACATTTT 60  
61 ATGCTTTACTAGCTATTGCTATTAATGTTAGGCAATGTCGTGCTCAATTTTACTTT 120  
61 ATGCTTTACTAGCTATTGCTATTAATGTTAGGCAATGTCGTGCTCAATTTTACTTT 120  
121 GTGGACAGAAATCTTAGACATGGAAGTAATCTTTTCTTAACTTGCCCATTCGAC 180  
121 GTGGACAGAAATCTTAGACATGGAAGTAATCTTTTCTTAACTTGCCCATTCGAC 180  
181 TTCTTTGGGGTGCAATTCCTCTGTACATACCTCTCCGCTGACTACTGACT 240  
181 TTCTTTGGGGTGCAATTCCTCTGTACATACCTCTCCGCTGACTACTGACT 240  
241 TCTGAAAGCAAGCTTGTTGATTTTGGCTCAATTAAGTATTTATGTAACAGACT 300  
241 TCTGAAAGCAAGCTTGTTGATTTTGGCTCAATTAAGTATTTATGTAACAGACT 300  
301 GTGTATTAATTTGCTCTCATGCTACGATGCTACAGTCACTCAATGCTGCTG 360  
301 GTGTATTAATTTGCTCTCATGCTACGATGCTACAGTCACTCAATGCTGCTG 360  
361 TATAGAGCTCAGACCTCTGCGACCTGGAATAATGCTACTCAGATGCTGCTG 420  
361 TATAGAGCTCAGACCTCTGCGACCTGGAATAATGCTACTCAGATGCTGCTG 420  
421 TTCTCTTCATGACAAATGGGCGATGATTTGATTTGACACTCTTGCGACAAAT 480  
421 TTCTCTTCATGACAAATGGGCGATGATTTGATTTGACACTCTTGCGACAAAT 480  
481 ACAGAAATGGAACCTTGATTTTAAAAAAGTGTACTTCTCTCTCAATCATTTAT 540  
481 ACAGAAATGGAACCTTGATTTTAAAAAAGTGTACTTCTCTCTCAATCATTTAT 540  
541 GAATTCCTGATCCCATCTTGTAGTGTCTTATTTTCAAGGCGCATATTACTG 600  
541 GAATTCCTGATCCCATCTTGTAGTGTCTTATTTTCAAGGCGCATATTACTG 600  
601 TGGAAAGCAGAGAAATCTGAGAGGTGCTCAGCCACCTCTGATCTGCTGCT 660

Db 601 TGGAAACGAGAGAACTGAGCAGTGCCTCAGCACCTGTACTCCCTCTGACTCTTC 660  
Qy 661 AGAGAGACCAAGCACTCTCTGACAGAGACCCGATTCAGGGGCACTGCGACGA 720  
Db 661 AGAGAGACCAAGCACTCTCTGACAGAGACCCGATTCAGGGGCACTGCGACGA 720  
Qy 721 CGGAAAGAAACAACCTGCTCTCTTGGTTCAGACGACGAGAAAGAGACGCTCTTG 780  
Db 721 CGGAAAGAAACAACCTGCTCTCTTGGTTCAGACGAGAGAAAGAGACGCTCTTG 780  
Qy 781 TTTTCATAGAAGACCTACAAAGAACAGCAATGTATGCTTCCAAATAGGCTCTCTCC 840  
Db 781 TTTTCATAGAAGACCTACAAAGAACAGCAATGTATGCTTCCAAATAGGCTCTCTCC 840  
Qy 841 CACTCAGATTCCTGCTCTTTCAGCAAGAGAAACATATGCACTTTTCAGAGCAGGAAA 900  
Db 841 CACTCAGATTCCTGCTCTTTCAGCAAGAGAAACATATGCACTTTTCAGAGCAGGAAA 900  
Qy 901 TTAGCCAAAGTCACTGAGCACTCTTACAGAGCTTTTGCCATTTGGGCTCCATATTC 960  
Db 901 TTAGCCAAAGTCACTGAGCACTCTTACAGAGCTTTTGCCATTTGGGCTCCATATTC 960  
Qy 961 CTGACTACAGTTATCTACTCAATTTTCTGAAAGAACTTGAATAATCAACTGTATC 1020  
Db 961 CTGACTACAGTTATCTACTCAATTTTCTGAAAGAACTTGAATAATCAACTGTATC 1020  
Qy 1021 CATACGCTCTTTGGCTCCAGTGTCAATTCCTTTGTATATCCCTTTTGTATCATTTG 1080  
Db 1021 CATACGCTCTTTGGCTCCAGTGTCAATTCCTTTGTATATCCCTTTTGTATCATTTG 1080  
Qy 1081 TGTCACAAAAGTTTTCAGAAAGCTTCTGAAATATCTCTGTGAGAGGCAATCCAG 1140  
Db 1081 TGTCACAAAAGTTTTCAGAAAGCTTCTGAAATATCTCTGTGAGAGGCAATCCAG 1140  
Qy 1141 CCACCAACACCGCTCAATATCCACTTGA 1170  
Db 1141 CCACCAACACCGCTCAATATCCACTTGA 1170

RESULT 3  
US-10-626-398-7  
Sequence 7, Application US/10626398  
Publication No. US20050074841A1  
GENERAL INFORMATION:  
APPLICANT: Lovemberg, Timothy  
APPLICANT: Liu, Changlu  
TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype  
FILE REFERENCE: PRD-0034  
CURRENT APPLICATION NUMBER: US/10/626,398  
PRIOR FILING DATE: 2003-07-23  
PRIOR APPLICATION NUMBER: 09/790,849  
PRIOR FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 60/208,260  
PRIOR FILING DATE: 2000-05-31  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 7  
LENGTH: 1170  
TYPE: DNA  
ORGANISM: Cavia porcellus  
US-10-626-398-7

Query Match 100.0%; Score 1170; DB 21; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGGCAAAATTAACATGATCGCTTAACATCAATTAATTTCTTGAATTTTA 60  
Db 1 ATGTGGCAAAATTAACATGATCGCTTAACATCAATTAATTTCTTGAATTTTA 60  
Qy 61 ATGTCTTAACTAGCTATTTGCTATATGTTAGCAATGTCGTGCTATTTAGCTTTAT 120  
Db 61 ATGTCTTAACTAGCTATTTGCTATATGTTAGCAATGTCGTGCTATTTAGCTTTAT 120

Db 61 ATGTCTTAACTAGCTATTTGCTATATGTTAGCAATGTCGTGCTATTTAGCTTTAT 120  
Qy 121 GTGACAGAAATTTAGACATCGAAGTAATTAATTTTCTTAACTTGGCATTGACAG 180  
Db 121 GTGACAGAAATTTAGACATCGAAGTAATTAATTTTCTTAACTTGGCATTGACAG 180  
Qy 181 TTTCTTGGGTGCAATTCGATTCCTGTATACATACCTTCTCGGTGACTTACTGGACT 240  
Db 181 TTTCTTGGGTGCAATTCGATTCCTGTATACATACCTTCTCGGTGACTTACTGGACT 240  
Qy 241 TCTGAAAGCAGCTTGTATTTTGGCTTCAATTAAGTCACTATCTTTTATAGACATCT 300  
Db 241 TCTGAAAGCAGCTTGTATTTTGGCTTCAATTAAGTCACTATCTTTTATAGACATCT 300  
Qy 301 GTGTATTAATTTGTCTCATACGCTACAGATGCTTACAGACATCAATATGCGGTGG 360  
Db 301 GTGTATTAATTTGTCTCATACGCTACAGATGCTTACAGACATCAATATGCGGTGG 360  
Qy 361 TATAGAGCTCAGCACTGCGCACCTGAAAAATGCTACTCAGATGCTGCTTTGGATA 420  
Db 361 TATAGAGCTCAGCACTGCGCACCTGAAAAATGCTACTCAGATGCTGCTTTGGATA 420  
Qy 421 TTCTCTTCAATGCAAAATGGGCGGATGATTTCTGATTTCAAGCTTTTGGCAATAGCACT 480  
Db 421 TTCTCTTCAATGCAAAATGGGCGGATGATTTCTGATTTCAAGCTTTTGGCAATAGCACT 480  
Qy 481 ACAGAAATGMAACCTGATTTTAAAAAGTGTACTTTGCTCTCCCTACATATTAATG 540  
Db 481 ACAGAAATGMAACCTGATTTTAAAAAGTGTACTTTGCTCTCCCTACATATTAATG 540  
Qy 541 GAATTCCTGATCCCATCTTGTATGTTGCTTATTTAGCGGCCCATATTTACTGAGCTG 600  
Db 541 GAATTCCTGATCCCATCTTGTATGTTGCTTATTTAGCGGCCCATATTTACTGAGCTG 600  
Qy 601 TGGAAACGAGAGAACTGAGCAGTGCCTCAGCACCTGTATCTCCCTGTGACTCTTCC 660  
Db 601 TGGAAACGAGAGAACTGAGCAGTGCCTCAGCACCTGTATCTCCCTGTGACTCTTCC 660  
Qy 661 AGCAGTACCAAGCACTCTCTGACAGAGACCCGATTCAGGGGCACTGTGCGACGA 720  
Db 661 AGCAGTACCAAGCACTCTCTGACAGAGACCCGATTCAGGGGCACTGTGCGACGA 720  
Qy 721 CGGAAAGAAACAACCTGCTCTTCTTGGTTCAGACATGCAAGAGAAAGAGACGCTCTTG 780  
Db 721 CGGAAAGAAACAACCTGCTCTTCTTGGTTCAGACATGCAAGAGAAAGAGACGCTCTTG 780  
Qy 781 TTTTCATAGAAGACCTACAAAGAACAGCAATGTATGCTTCCAAATAGGCTCTCTCC 840  
Db 781 TTTTCATAGAAGACCTACAAAGAACAGCAATGTATGCTTCCAAATAGGCTCTCTCC 840  
Qy 841 CACTCAGATTCCTGCTCTTTCAGCAAGAGAAACATATGGAATTTTCAGAGCAGGAAA 900  
Db 841 CACTCAGATTCCTGCTCTTTCAGCAAGAGAAACATATGGAATTTTCAGAGCAGGAAA 900  
Qy 901 TTAGCCAAAGTCACTGAGCACTCTTACAGAGCTTTTGCCATTTGGGCTCCATATTC 960  
Db 901 TTAGCCAAAGTCACTGAGCACTCTTACAGAGCTTTTGCCATTTGGGCTCCATATTC 960  
Qy 961 CTGACTACAGTTATCTACTCAATTTTCTGAAAGAACTTGAATAATCAACTGTATC 1020  
Db 961 CTGACTACAGTTATCTACTCAATTTTCTGAAAGAACTTGAATAATCAACTGTATC 1020  
Qy 1021 CATACGCTCTTTGGCTCCAGTGTCAATTCCTTTGTATATCCCTTTTGTATCATTTG 1080  
Db 1021 CATACGCTCTTTGGCTCCAGTGTCAATTCCTTTGTATATCCCTTTTGTATCATTTG 1080  
Qy 1081 TGTCACAAAAGTTTTCAGAAAGCTTCTGAAATATCTCTGTGAGAGGCAATCCAG 1140  
Db 1081 TGTCACAAAAGTTTTCAGAAAGCTTCTGAAATATCTCTGTGAGAGGCAATCCAG 1140  
Qy 1141 CCACCAACACCGCTCAATATCCACTTGA 1170  
Db 1141 CCACCAACACCGCTCAATATCCACTTGA 1170

RESULT 4  
US-09-812-216-1  
; Sequence 1, Application US/09812216  
; Patent No. US20020098539A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsema, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CNO1069  
; CURRENT APPLICATION NUMBER: US/09/812,216  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 09/414,010  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-812-216-1

Query Match 57.7%; Score 675; DB 9; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 5,9e-185;

Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATACAGTACAAATCGCTTACATCAATTAATTTCTTGAACATTTTAATGCTT 67  
DB 11 CTAATAGACATCAATTATACAGACGCGTTACTTTAGCATTTTATAGTCTT 70  
QY 68 TACTAGCTATTGCTTAATGTTAGGCAATGCTGCTCATTTTATGTTAGGACA 127  
DB 71 TAGTAGCTTTGCTTAATGCTAGGAAATGCTTGGTCAATTTTGTGTTGAGACA 130  
QY 128 GAATCTTAGACATGAGTAATTAATTTTCTTAACTTGGCAGTGGAGCTTCTTG 187  
DB 131 AAAACCTTAGACATGAGTAATTTTCTTAACTTGGCAGTGGAGCTTCTTG 190  
QY 188 TGGGTGCAATTCCTCTGTAATACCTTCTGCTGCACTTACTGAGCTTCTGGA 247  
DB 191 TGGGTGTAATTCCTGTAATACCTTCTGCTGCACTTACTGAGCTTCTGGA 250  
QY 248 AGCAAGCTTGTATTTGGCTGATTAATGCTGATTAATGCTGATTAATGCTGATTA 307  
DB 251 AGCAAGCTTGTATTTGGCTGATTAATGCTGATTAATGCTGATTAATGCTGATTA 310  
QY 308 ATATGCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 367  
DB 311 ACATGCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 370  
QY 368 CTCAGACCTTGGCACTGGAATTTGCTGATGCTGATGCTGATGCTGATGCTGAT 427  
DB 371 CTCAGACCTTGGCACTGGAATTTGCTGATGCTGATGCTGATGCTGATGCTGAT 430  
QY 428 TCATGACAAATGGCGGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 487  
DB 431 TCTTAGTGAATGGCGGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 490  
QY 488 GTGAACCTGGATTTTAAAGAGTGTACTTGTCTCCCTGATCATTAATGGAATCC 547  
DB 491 GTGAACCTGGATTTTAAAGAGTGTACTTGTCTCCCTGATCATTAATGGAATCC 550  
QY 548 TGATCCCATCTTTGTTAGTCTTATTTGAGCGCCATATTTACTGAGCCTGTGGAAGC 607  
DB 551 TGATCCCATCTTTGTTAGTCTTATTTGAGCGCCATATTTACTGAGCCTGTGGAAGC 610  
QY 608 GAGAGAACTGACAGGTGCTTACAGCACCCTGTAATCCCTCTGATCTTCCAGCAGTG 667

DB 611 GTGATCATCTCAGTAGGTCAGCAAGGCCATCTGATCACTGCTGTCTTCCAAACA--- 667  
QY 668 ACCAGGACATCTCCGTCAGACAGAGACCCGATTTCAAGGCGCATCTGCGACAGCAAG 727  
DB 668 TCTGTGACACTCATTTCAAGAGTACATATCTTCAAGAGATCTTTCTGTGATGACAG 727  
QY 728 AAACAACTGCTCTTCTGTTTCAAGATCAAGTCAAGGAGAAAGAGCATCTTGTGTTTCCA 787  
DB 728 AAGTCTGATCTTCTTATTCATTCAGAGACAGAGAAAGAGTGTCTCATGTTTCTT 787  
QY 788 TAAAGCCTTAAAGAACGATGATGATGCTTCCAAATAGGCTTCTTCCACTCAG 847  
DB 788 CAAGAACCAATGAAATGCAATCAATGCTTCCAAATAGGCTTCTTCCACTCAG 847  
QY 848 ATTCCTGCTCTTCAAGAAAGGAACTATGATGATGCTTCCAGACCCAGAAATAGCCA 907  
DB 848 ATTCCTGCTCTTCAAGAAAGGAACTATGATGATGCTTCCAGACCCAGAAATAGCCA 907  
QY 908 AGTCACTGGCCATCTCTTAGGGGTTTGTGCTTGTGCTGGGCTCCATATCTCTGTTCA 967  
DB 908 AGTCACTGGCCATCTCTTAGGGGTTTGTGCTTGTGCTGGGCTCCATATCTCTGTTCA 967  
QY 968 CAGTATCTACTCATTTTCTGTAAGAACTTGAATCACTGTAACCTGTAACCTGTA 1027  
DB 968 CAGTATCTACTCATTTTCTGTAAGAACTTGAATCACTGTAACCTGTAACCTGTA 1027  
QY 1028 CTTTGGCTCAGAGTGTGATTCCTTGTATTCCTTTTGTATTCATTTGTTGATGTA 1087  
DB 1028 CATTGCTCAGAGTGTGATTCCTTGTATTCCTTTTGTATTCATTTGTTGATGTA 1087  
QY 1088 AACGTTTCAAGAGCTTCTGAAATATCTTCTGTAAGAAAGCAATTCACGCCAACC 1147  
DB 1088 AGCGCTTCAAGAGCTTCTGAAATATCTTCTGTAAGAAAGCAATTCACGCCAACC 1147  
QY 1148 ACAACCG 1154  
DB 1148 AACACAG 1154

RESULT 5  
US-09-910-411-1  
; Sequence 1, Application US/09910411  
; Patent No. US20020137054A1  
; GENERAL INFORMATION:  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Fitzgerald, Laura  
; APPLICANT: Li, Xialong  
; APPLICANT: Michalovich, David  
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor  
; FILE REFERENCE: GP70655-2C1  
; CURRENT APPLICATION NUMBER: US/09/910,411  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: 09/693,761  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/497,790  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/431,898  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-910-411-1

Query Match 57.7%; Score 675; DB 9; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 5,9e-185;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATACAGTACAAATCGCTTACATCAATTAATTTCTTGAACATTTTAATGCTT 67

11 CTAAATGCAATCAATTTATGCTAGAGCTGCTGTTACTTAGCATTTTATATGCTC 70  
68 TACTAGCTATTGCTAATAATGTTAGGCAATGCTGCTCATTTAGCTTTTATGTGACA 127  
71 TAGTAGCTTTTGTATAATGCTAGGAAAGCTTTGCTCATTTTAAAGCTTTTGTGTGAGCA 130  
128 GAAATCTTGACATGCAAGTAATTTACTTTTCTTAACTTGGCATTGAGACTTCTTGG 187  
131 AAAACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCATTCTGACTTCTTGG 190  
188 TGGGTGCAATGCAATTCCTCTGTACATACCTTCTGCTGACTTAACTGCACTTCTGAA 247  
191 TGGGTGCTGATCTTCATCTCTTGTATACCTCCACAGGCTGTTGCAATGGAGATTGGAA 250  
248 ACCAAGCTTGTATTTTGGCTCATTAAGTACATCTTTTATATGACATCTGTATTA 307  
251 AGGAAATCTGTATTTTGGCTCATTAAGTACATCTTTTATGATACAGATCTGTATTA 310  
308 ATATTGCTCATCTACATGATCGCTACAGTCAAGTCAAAATGCGGTGTATAGAG 367  
311 AATTTGCTCATCTACATGATCGCTACATGATCGCTACATGATCGCTGTATATAGAA 370  
368 CTCAGCATCTGAGCACTGGAATTTGCTACTAGATGCTGCTGTTGATATCTCT 427  
371 CTCACATATCTGGGCTTGAAGATTGTTACTGTATGCTGATGCTGCTGCTGCTGCT 430  
428 TCATGCAAAATGGGCGGATGATTTGATTTGACATCTTTGGCAATTAGCATACGAAT 487  
431 TCTTAGTGAATGGGCGGATGATTTGATTTGACATCTTTGGCAATTAGCATACGAAT 490  
488 GTGAACCTGGAATTTTAAAGTGTACTTGTCTCCCTACATATTTAGGAATTC 547  
491 GTGAACCTGGAATTTTGTGGAATGATATCTTCCCTACATATTTTGAATTCG 550  
548 TGATCCCATCTTGTAGTGTATTTTGAAGCGCCATATTTAGTGAAGCTGTGAAAG 607  
551 TGATCCCATCTTGTAGTGTATTTTGAAGCGCCATATTTAGTGAAGCTGTGAAAG 610  
608 GAGAGAAATGAGAGAGTGTCTGACGCACTTCTGCTGCTGCTGCTGCTGCTGCTG 667  
611 GTGATCATCTGATGATGCTGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 667  
668 ACCAGGACATCTGCTGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 727  
668 TCTGCTGCACTTCAATGAGGATGATCTTCTGCAAGAGATCTTCTGCTGCTGCAAG 727  
728 AAACAATGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 787  
728 AAGTCTGCTGCTGCTTCAATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 787  
788 TAAAGACCTCAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 847  
788 CAAAGACCTCAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 847  
848 ATTCCCTGCTGCTGCAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907  
848 ATTCTGCTGCTGCTGCAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907  
908 ACTGACTGCTGCTGCTGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967  
908 ACTGACTGCTGCTGCTGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967  
968 CAGTATCTGCTGCTGCTGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1027  
968 CAGTATCTGCTGCTGCTGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1027  
1028 CATTGCTGCTGCTGCTGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1087  
1028 CATTGCTGCTGCTGCTGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1087  
1088 AACGTTTCAAGAGAGCTGCTGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1147  
1088 AACGTTTCAAGAGAGCTGCTGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1147

Db 1088 AGCGCTTCAAAAGCTTCTTGAATAATTTTGTATATAAAGCAACTTACATCAC 1147  
Qy 1148 ACAACG 1154  
Db 1148 AACACG 1154

RESULT 6  
US-09-875-076-13  
; Sequence 13, Application US/09875076  
; Publication No. US20030017528A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/09/875,076  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,633  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,293  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-875-076-13

Query Match 57.7%; Score 675; DB 10; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 5,9e-185;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATTAACGATACATCCGCTTAACATCAATTAATTTCTTTGACATTTTAAATGCTT 67  
DB 11 CTAATAGACAAATCAATTTATATCACTAGACATCGTGTTACTTACATTTTATATGCTT 70  
QY 68 TACTAGCTATTGCTTAATTTAGGCAATGTCGTGCTATTTAGCTTTTATTTGAGACA 127  
DB 71 TAGTAGCTTTTGTATTAATGCTAGGAAATGCTTGGTATTTAGCTTTTGTGGTGACA 130  
QY 128 GAAATCTTAGACATGAGATTAATTTCTTTTCTTAACCTGGGCACTGGACGCTTCTTG 187  
DB 131 AAACCTTAGACATGAGATTAATTTTCTTTTCTTAACCTGGGCACTTGGACCTTCTTG 190  
QY 188 TGGGTGCAATTCGAATTCCTCTGATACATCTTCTCTGCTGACCTTACTGACCTTGGAA 247  
DB 191 TGGGTGATCTCCATTCCTTTGATCATCCCTCAACACGCTGTGCAATGGGATTTTGAA 250  
QY 248 AGCAAGCTTGTGATTTTGGGCTCATCTGACATCTTTTATGTAACGATCTGTGATA 307  
DB 251 AGGAATCTGTGATTTTGGGCTCATCTGACATCTTGTATGTAACGATCTGTGATA 310  
QY 308 ATATGCTCATGAGCTACGATGCTACGATGCTACGATGCTACGATGCTACGATGCTACG 367  
DB 311 ACATTTCTCATGAGCTACGATGCTACGATGCTACGATGCTACGATGCTACGATGCTACG 370  
QY 368 CTGACACTGCGACCTGGAATAATGCTACCTGATGATGCTGCTGCTGCTGCTGCTGCT 427  
DB 371 CTCAACATAGCTGGGGCTTTGAAAGATTTGATCTGATGATGCTGCTGCTGCTGCTGCT 430  
QY 428 TCATGACAAATGGGCGGATGATTTGATTTGACATCTTTGACAAATGACACTACAGAT 487  
DB 431 TCTTAGTAATGGGCGGATGATTTGATTTGACATCTTTGACAAATGACACTACAGAT 490  
QY 488 GTGAACCTGGAATTTTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547  
DB 491 GTGAACCTGGAATTTTTCGGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550  
QY 548 TGATCCCATCTTGTAGCTTATTTCAAGCGCCATATTTACTGAGCCCTGGAAGC 607  
DB 551 TGATCCCATCTTGTAGCTTATTTCAACATGATATTTATTTGAGCGCTGGAAGC 610  
QY 608 GAGAGAACTGAGCGGCTGCTGAGCGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667  
DB 611 GTGATCATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667  
QY 668 AACGAGCACTCTGCGACAGACAGACCCGATTTCAAGGGCGCATCTGCGACAGGAAAG 727  
DB 668 TCTGAGCACTCTGCGACAGAGTATCTTCAAGAGATCTTCTGCTGCTGCTGCTGCTGCT 727  
QY 728 AAAACACTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787  
DB 728 AAGTCTCTGATCTCTTCAATTCAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787  
QY 788 TAAAGCCTTAAGAAAGCAATGATGCTTCCAAATGAGGCTCTCTCTCTCTCTCTCTCT 847  
DB 788 CAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 847  
QY 848 ATTCCCTGCTCTTCTGAGCAAGGAAATATGCACTTTTCAAGCCAGGAAATAGGCA 907  
DB 848 ATTCTGTAGCTCTTCAAGGAGGAAATGTTGAATCTGTTAGAGCCAGGAGATTAGCA 907  
QY 908 AGTCACTGGCAATCTTTAGCAAGCTTTTGGCAATTTGCTGAGGCTCATATTTCACTG 967  
DB 908 AGTCACTGGCAATCTTTAGCAAGCTTTTGGCAATTTGCTGAGGCTCATATTTCACTG 967  
QY 968 CAGTATCTACATCTTTTCTGAAAGAACTTCAATTAATCACTGTTACTGCTACTG 1027  
DB 968 CAATTTCTCTTCAATTTATCTGAGCAAGGCTCTTAAATCAATTTGATAGAAATG 1027  
QY 1028 CTTTGGCTCCAGTGGTCAATCTTCTTGTATCTCTTTTGTATCAATTTGCTGCA 1087  
DB 1028 CATTTGGCTTCAAGTGGTCAATCTTCTTGTATCTCTTTTGTATCAATTTGCTGCA 1087

QY 1088 AACCTTTGAGAGGCTTTCTGAAATACTTCTGAGAGAGGCAATCCAGCCACAC 1147  
DB 1088 AGCGCTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAACCTTACCATC 1147  
QY 1148 ACAACCG 1154  
DB 1148 AACACAG 1154  
RESULT 7  
US-09-876-252-13  
Sequence 13, Application US/09876252  
Publication No. US20030018182A1  
GENERAL INFORMATION:  
APPLICANT: Behan, Dominic P.  
APPLICANT: Lehmann-Brinma, Karin  
APPLICANT: Chalmers, Derek T.  
APPLICANT: Lowitz, Kevin P.  
APPLICANT: Lin, I-Lin  
APPLICANT: Dang, Huang T.  
APPLICANT: Chen, Ruoping  
APPLICANT: Liaw, Chen W.  
TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Receptor  
FILE REFERENCE: AREN-0054  
CURRENT APPLICATION NUMBER: US/09/876, 252  
CURRENT FILING DATE: 2001-06-07  
PRIOR APPLICATION NUMBER: 09/416,760  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: 09/170,496  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: 60/110,060  
PRIOR FILING DATE: 1998-11-27  
PRIOR APPLICATION NUMBER: 60/120,416  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 60/121,852  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/109,213  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: 60/123,944  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,945  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,946  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,949  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/152,524  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: 60/151,114  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: 60/108,029  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: 60/136,436  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,439  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,567  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/137,127  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/137,131  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/141,448  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 60/136,437  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/156,555  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,634

PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,653  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/157,280  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,294  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,281  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,282  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/156,633  
PRIOR FILING DATE: 1999-09-29  
NUMBER OF SEQ ID NOS: 146  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 13  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-876-252-13

Query Match 57.7%; Score 675; DB 10; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 5,9e-185;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

8 CAAATAACGATACATCGCCTTAACATCAATTAATTTCTTGACATTTTAAATGCTT  
11 CTAAATGACACATCAATTTATCACTAGACCTGCTGTTACTTTAGCAATTTTATGCTT  
68 TACTAGCTATTGCTATATGTTAGGCAATGCTGCTGCTATTTAGCTTTATTTAGGACA  
71 TAGTACTTTTGTATATATAGCTAGAAATGCTTTGCTATTTAGCTTTTGTGTGGACA  
128 GAAATCTTGAACATCGAAGTAATTAATTTCTTTAACTTTGGCCATTTGACATTTCTT  
131 AAAACCTTGAACATCGAAGTAATTTCTTTAACTTTGGCCATTTGACATTTCTTCTT  
188 TGGGTCATTTGCAATTTCTCTGATACATCTTCTGAGCTTTGACATTTCTTCTT  
191 TGGGTGATCTTCATTTCTTTGATACATCTTCTGAGCTTTGACATTTCTTCTTCTT  
248 AGCAACCTTGTATTTTGGCTCATTAAGTATCTTTTATTTAGTATCTTGTATTA  
251 AGGAATCTGTATTTTGGCTCATTAAGTATCTTTTATTTAGTATCTTGTATTA  
308 AATTTGCTCATCTGATGATGCTGATCACTGATCTCAATGCTGCTGTATTAAG  
311 ACATTTCTCATCTGATGATGCTGATCACTGATCTCAATGCTGCTGTATTAAG  
368 CTCAGACCTTGGCACTGGAATTTGCTATCTGATGCTGCTGCTGCTGCTGCTGCT  
371 CTCAGACCTTGGCACTGGAATTTGCTATCTGATGCTGCTGCTGCTGCTGCTGCT  
428 TCATGACAAATGGGCGATGATTTCTGATTTCAAGCTTTGGGAGAAATAGCACTA  
431 TCTTATGATGATGGGCGAATGATTTCTGATTTCAAGCTTTGGGAGAAATAGCACTA  
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491 GTGAACCTGATTTTAAAAAGTGTACTTTGCTCTCCCTACATCAATTTGAATTC  
548 TGAATCCCATCTTGTATTTGCTATTTGAGGCGCATTTATTTAGAGCTTGTGAAG  
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608 GAGAGAAATGAGCAGGTGCTGAGCACTGCTGATCTTCTGATCTTCCAGAGT  
611 GTGATCATCTCAATAGTGTGCAAGCACTGCTGATCTTCTGATCTTCCAGAGT  
668 ACCAGGACATCTCTGAGACAGAGCCGATTTCAAGGCGCATTTGCGACAGAGAG  
668 TGTGTGATCTTCATTTCTTGTATCTTCAAGGAGATCTCTTTCTGACATCGACAG

728 AAACAATGCTCTCTTGGTTTCAAGACATGACAGAGAAAGACATCTTCTTTTCA  
728 AAGTCTCTGATCTTCAATTTCAAGAGACAGAGAGAAAGATGATCTTCTTCTTCT  
788 TAAAGCTTCAAGAAACAGCATGATGATGCTTCAAAATGGCTTCTTCCACTGAG  
788 CAAGAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT  
848 ATTCCCTGCTCTTCAAGAAAGGAAATATGATGATGATGATGATGATGATGATGAT  
848 ATTCTGATCTTCAAGAAAGGAAATATGATGATGATGATGATGATGATGATGATGAT  
908 AGTCACTGACATCTTCTTCAAGAGCTTCTTCAAGAGCTTCTTCAAGAGCTTCTT  
908 AGTCACTGACATCTTCTTCAAGAGCTTCTTCAAGAGCTTCTTCAAGAGCTTCTT  
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968 CAGTATCTATCTATTTTCTGAAAGGAACTTCAATCAATCAATCAATCAATCAAT  
1028 CTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
1028 CATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
1088 AACGTTTCAAGAGCTTCTTCAAGAGCTTCTTCAAGAGCTTCTTCAAGAGCTTCT  
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1148 ACAACG 1154  
1148 AACACAG 1154

RESULT 8  
US-10-052-193-1  
Sequence 1, Application US/10052193  
Publication No. US20020132755A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer, Inc.  
TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS  
FILE REFERENCE: PCT/0963A  
CURRENT APPLICATION NUMBER: US/10/052,193  
CURRENT FILING DATE: 2002-01-17  
PRIOR APPLICATION NUMBER: 0101223.6  
PRIOR FILING DATE: 2001-01-17  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-052-193-1

Query Match 57.7%; Score 675; DB 13; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 5,9e-185;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

8 CAAATAACGATACATCGCCTTAACATCAATTAATTTCTTGACATTTTAAATGCTT  
11 CTAAATGACACATCAATTTATCACTAGACCTGCTGTTACTTTAGCAATTTTATGCTT  
68 TACTAGCTATTGCTATATGTTAGGCAATGCTGCTGCTATTTAGCTTTATTTAGGACA  
71 TAGTACTTTTGTATATATAGCTAGAAATGCTTTGCTATTTAGCTTTTGTGTGGACA  
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131 AAAACCTTGAACATCGAAGTAATTTCTTTAACTTTGGCCATTTGACATTTCTTCTT  
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248 AGCAAGCTGTGTATTTGGCTCATTTACTGACTATCTTTATGTAAGAGCATGTGTATA 307
251 AGGAATCTGTGTATTTGGCTCAGTACTGACTATCTTTATGTAAGAGCATGTGTATA 310
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311 ACATTGTCTCATCAGCTACGTAACGTCGTAACAGTCTCAAAATGCGGTGTATAG 370
368 CTCAGCACTGTGGCAGCTGGAATAATGCTACTCAGATGCTGTTGGATATCTCT 427
371 CTCACATACATGGGCTTTGAAGATTTGTAATCTGATGCTGAGTGGCTGGCT 430
428 TCATGACAAATGGGCGATGATTTGATTTGAGTCTGAGTCTGAGAAATAGCAAT 487
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488 GTGAACCTGTGATTTTAAAGTGTACTTGTCTCTCCCTCATCATCTATTTGAATTC 547
491 GTGAACCTGTGATTTTTCGGAATGTGTATCTTGCATCATCATCTATTTGAATTC 550
548 TGATCCCATCTTGTAGTGTCTTATTTGAGGCGCCATTTACTGAGCTGTGGAAG 607
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608 GAGAGAACTGAGCAGGTGCTCAGCCACCTGTACTCTCCCTGTGACTTTTCAGCAGTG 667
611 GTGATCATCTCAGTAGTGCCAAAGGCGATCTGAGTCTGCTGTCTTCCACA--- 667
668 AGCAGGACATCTTCGAGACAGACCCCGATTTCAAGGCGCTGTGCGACAGCGAAG 727
668 TCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTTCTGTGATGACG 727
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1148 ACAACCG 1154
1148 AACACAG 1154

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## RESULT 9

US-10-272-983-13  
 ; Sequence 13, Application US/10272983  
 ; Publication No. US20030148450A1

## GENERAL INFORMATION:

APPLICANT: Chen, Ruoping  
 APPLICANT: Dang, Huong T.  
 APPLICANT: Liaw, Chen W.

```

APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/10/272,983
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-10-272-983-13

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Query Match 57.7%; Score 675; DB 15; Length 1173;

Best Local Similarity 74.9%; Pred. No. 5,9e-185;

Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

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8 CAATATACATGATCCCTTAAATCAATTAATTTCTTGAATTTTAAATGCTT 67
11 CTAATAGCAATCAATTTATCACTAGACATCGTGTACTTTAGATTTTATGCTT 70
68 TACTAGCTATTTGCTTAAATGTTAGGCAATGTCGTGCTATTTTAACTTTTATG 127
71 TAGTAGCTTTGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATG 130
128 GAAATCTTACATGAGATGATTTCTTTTCTTAACTTGGCCATGAGCTTTCTT 187
131 AAAACCTTACATGAGATGATTTCTTTTCTTAACTTGGCCATGAGCTTTCTT 190
188 TGGGTGCAATGCAATTCCTCTGTACATACCTTCTGCTGACTTAACTGACTG 247
191 TGGGTGCAATGCAATTCCTCTGTACATACCTTCTGCTGACTTAACTGACTG 250
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251 AGGAATCTGTGTATTTGGCTCAGTACTGACTATCTTTATGTAAGAGCATG 310
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428 TCATGACAAATGGGCGATGATTTGATTTGAGTCTGAGTCTGAGAAATAGCAAT 487
431 TCTTAGTAATGGGCGAATGATTTGATTTGAGTCTGAGTCTGAGAAATAGCAAT 490
488 GTGAACCTGTGATTTTAAAGTGTACTTGTCTCTCCCTCATCATCTATTTGA 547
491 GTGAACCTGTGATTTTTCGGAATGTGTATCTTGCATCATCATCTATTTGA 550

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APPLICANT: Liaw, Chen W.  
APPLICANT: Lowitz, Kevin  
APPLICANT: Chalmers, Derek T.  
APPLICANT: Behan, Dominic P.  
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
FILE REFERENCE: 7.US28.CON  
CURRENT APPLICATION NUMBER: US/10/417,820A  
CURRENT FILING DATE: 2003-04-16  
PRIOR APPLICATION NUMBER: 09/416,760  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: 09/170,496  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: 60/110,060  
PRIOR FILING DATE: 1998-11-27  
PRIOR APPLICATION NUMBER: 60/120,416  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 60/121,852  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/109,213  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: 60/123,944  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,945  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,948  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,951  
PRIOR FILING DATE: 1999-03-12  
Remaining prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 13  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-417-820A-13

Query Match 57.7%; Score 675; DB 17; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 5.9e-185;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

QY 8 CAAATACAGTACATCGCTTAACATCAATTAATTTCTTGACATTTTATGCTT 67  
DB 11 CTAATGACACAAATTAATTAATCAAGACCTGCTTACTTATTAAGATTTTATGCTT 70  
QY 68 TACTAGCTTATGCTTAATGTTAGGCAATGCTGCTCATTTTATGCTTATGCTT 127  
DB 71 TAGTACTTTTGTATATATGCTAGGAATGCTTGGTCATTTTATGCTTATGCTT 130  
QY 128 GAAATTTAGACATCGAATTAATTAATTTTCTTAATCTGGCATTTGACATTTCTTTG 187  
DB 131 AAAACCTTGACATCGAATTAATTAATTTTCTTAATCTGGCATTTGACATTTCTTTG 190  
QY 188 TGGGTGCAATTTGCTCTGTAACATCTTCTGCTGACATTTGACATTTGACATTTG 247  
DB 191 TGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250  
QY 248 AGCAAGCTTGTATTTTGGCTCATTAAGTACATTTTATGCTTATGCTTATGCTT 307  
DB 251 AGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 310  
QY 308 ATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367  
DB 311 ACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 370  
QY 368 CTCAGACTTGGCAGCTGGAATTTGCTACTCAGATGCTGCTGCTGCTGCTGCT 427  
DB 371 CTCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 430  
QY 428 TCATGCAAAATGGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487  
DB 431 TCTTAGTGAATGGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490

QY 488 GTGACCTGATTTTTAAAAAGNGTACTTGTCTCCCTACATCATTAATGGAATTC 547  
DB 491 GTGACCTGATTTTTTTTGGAAATGTAATCTCTGCTGCTGCTGCTGCTGCTGCT 550  
QY 548 TGAATCCCATCTTGTATGCTTATTTTCAAGCCCATATTTTATGCTGAGCTGGAAGC 607  
DB 551 TGAATCCCATCTTGTATGCTTATTTTCAAGCCCATATTTTATGCTGAGCTGGAAGC 610  
QY 608 GAGAGAACTGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667  
DB 611 GTATCATCTGATGAGTGTGCAAGGATCTGCTGCTGCTGCTGCTGCTGCTGCT 667  
QY 668 ACCAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727  
DB 668 TCTGTGACATCTATTTCAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 727  
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QY 1148 ACAACCG 1154  
DB 1148 AACACAG 1154

RESULT 13  
US-10-349-253A-1  
Sequence 1, Application US/10349253A  
Publication No. US20040043393A1  
GENERAL INFORMATION:  
APPLICANT: Ambart, Kelly  
APPLICANT: Bergsma, Derek  
APPLICANT: Fitzgerald, Laura  
APPLICANT: Graybill, Todd  
APPLICANT: Li, Xiaolong  
APPLICANT: Michalovich, David  
APPLICANT: Morrow, Dwight  
APPLICANT: Zhu, Yuan  
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor  
FILE REFERENCE: GP70655-2C2  
CURRENT APPLICATION NUMBER: US/10/349,253A  
CURRENT FILING DATE: 2003-01-21  
PRIOR APPLICATION NUMBER: 09/910,411  
PRIOR FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: 09/693,761  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 09/497,790  
PRIOR FILING DATE: 2000-02-03

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? PRIOR APPLICATION NUMBER: 09/431,896
? PRIOR FILING DATE: 1999-11-02
? NUMBER OF SEQ ID NOS: 2
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 1173
? TYPE: DNA
? ORGANISM: Homo sapien
? US-10-349-253A-1

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Query Match	57.7%	Score 675;	DB 18;	Length 1173;
Best Local Similarity	74.9%;	Pred. No. 5.9e-185;		
Matches 859;	Conservative	0;	Mismatches 285;	Indels 3;
				Gaps 12;

Qy	8	CAAAATACAGTCAATACGCGCTTAACATCAATAAAATTTCTTGACAATTTTAATGCTT	67
Dp	11	CTAATAGCAAAATCAATTTATCACTAAGACACTCGTGTACTTTAGCATTTTATATGCT	70
Qy	68	TACTACTATTTGCTATATATGTTAAGCCATATGCTGTGCTATTTTACCTTTATTTGTGACA	127
Dp	71	TACTACTCTTTTGTATATTAAGCTTAGGAAATGCTTGTGCTATTTTAGCTTTGTGTGACA	130
Qy	128	GAATCTTAGACATCGAAGTAATTACTTTTTCTTAATCTTGAGCCATTGCAGACTTTTG	187
Dp	131	AAAACCTTAGACATCGAAGTAATTTTCTTAATCTTGAGCCATCTGACTTTCTTG	190
Qy	188	TGGGTGCAAATTGCATTTCTCTGTACATACCTTCTGCTGACTTACTGACCTTGTGAA	247
Dp	191	TGGGTGTGATCTCCATTTCTTTGTACATCCCTGCACACCTGTTCGAATGGGATTTTGAA	250
Qy	248	AGAACCTGTGTATTTTGGCTCACTAATCTGAATATCTTTTATGTACAGATCTGTGATA	307
Dp	251	AGGAATCTGTGTATTTTGGCTCACTACTGACTAATCTGTATGTACAGACTGTGTATATA	310
Qy	308	ATATTGCTCATCACTACACTAGATCGCTACACAGTCAAGTCTCAATACCGTGTGTATAG	367
Dp	311	ACATTGTCTCATCACTACACTATGATTCGATCTGTCAAGTCTCAAAATGTCTGTCTTATAGAA	370
Qy	368	CTAGACATCTGTGGCACTTGAAAATTTGCTACTCAATGTGTGGCTTTTGATTTCTCT	427
Dp	371	CTCAACATACCTGGGGCTTTGAAAGATTTGTACTCTGATGTGTGGCGTTTGGGTGCTGGCCT	430
Qy	428	TCATGCAAAATGGGCGATGATTTCTGATTTGAGACTTTGGCAGAAATAGCACTACAGAT	487
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Qy	488	GTGAACCTGTGATTTTTAAAAAGGTGACTTGTGCTCTCCATACATTAATTAGGAATTC	547
Dp	491	GTGAACCTGTGATTTTTTGGAAATGGTACATCTTGCATACATCAATTTCTTGGAAATTCG	550
Qy	548	TGATCCCAATCTTGTAGTTGCTTAATTCAGGCGCCATTAATTAATCGAGCCTGTGGAAG	607
Dp	551	TGATCCCAATCTTGTAGTTGCTTAATTCAGGCGCCATTAATTAATTAATTAATTAATTAAT	610
Qy	608	GAGAGAACTGAGCAGGTGCTTCAGCACTCTGACTCCCTCTGACTCTTCAGCAGTGT	667
Dp	611	GTGATCATCTCAGTAGGTGCTCAAAAGCAATCCGAGCTGACTGCTGTCTCTTCCAAAC--	667
Qy	668	ACCAAGCACTCTCTGCAAGACAGAACCCGATTTAAGGCGCACTCTGCACAGCAAG	727
Dp	668	TCTGTGGAACCTCATTCAGAGGTGACATATCTTCAAGAGATCTCTTCTGCAATCGACAG	727
Qy	728	AAACAATGCTCTCTTGGTTACAGCAAGTCAAGGAGAAAGAGAGCTCTTGTGTTTCA	787
Dp	728	AAATCTCTGATCTCTTCAATCAAGAGACAGAGAGAAAGATGATCTCATGTGTTTCT	787
Qy	788	TAAAGCTTACAGAAACAGCAATGTGATGCTTCCAAATGGGCTTCTCTCCACTAG	847
Dp	788	CAAGAACAAGATGAATACCAATACAAATGCTTCCAAATGGGTTCTCTTCCCAATCAG	847
Qy	848	ATTCCCGGCTCTTTCAGAAAGGGAACATATGGAATTTTCAAGACCAAGAAATTAACCA	907
Dp	848	ATTCTGTAGCTCTTTCAGAAAGGGAACATGTTGAATCTTTCAGACCAAGGATTAACCA	907

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US-RESULT 14
US-10-723-955-13
Sequence 13, Application US/10723955
Publication No. US20040110238A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lin, I-Lin
APPLICANT: Liaw, Chen W.
APPLICANT: Lehman-Bruhlma, Karin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
FILE REFERENCE: 7, US29 .CON
CURRENT FILING DATE: 2003-11-26
PRIORITY APPLICATION NUMBER: US/10/723,955
PRIORITY FILING DATE: 2003-4-16
PRIORITY APPLICATION NUMBER: 09/416,760
PRIORITY FILING DATE: 1999-10-12
PRIORITY APPLICATION NUMBER: 09/170,496
PRIORITY FILING DATE: 1998-10-13
PRIORITY APPLICATION NUMBER: 60/110,060
PRIORITY FILING DATE: 1998-11-27
PRIORITY APPLICATION NUMBER: 60/120,416
PRIORITY FILING DATE: 1999-02-16
PRIORITY APPLICATION NUMBER: 60/121,852
PRIORITY FILING DATE: 1999-02-26
PRIORITY APPLICATION NUMBER: 60/109,213
PRIORITY FILING DATE: 1998-11-20
PRIORITY APPLICATION NUMBER: 60/123,944
PRIORITY FILING DATE: 1999-03-12
PRIORITY APPLICATION NUMBER: 60/123,945
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PRIORITY APPLICATION NUMBER: 60/123,948
PRIORITY FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
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LENGTH: 1173
TYPE: DNA
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Best Local Similarity 74.3%; Pred. No. 5; 9e-185;
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 16:34:25 ; Search time 3685 Seconds  
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Scoring table: IDENTITY\_NUC  
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_esc3:\*  
4: gb\_esc4:\*  
5: gb\_esc5:\*  
6: gb\_esc6:\*  
7: gb\_esc7:\*  
8: gb\_esc8:\*  
9: gb\_esc9:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	410.6	35.1	704	7	CF147821 AGENCOURT
3	233	19.9	721	7	CO959034 AGENCOURT
4	127.8	10.9	853	6	CD326085 AGENCOURT
5	112	9.6	672	6	CB556920 AMGNNUC:U
6	109.2	9.3	732	7	CF147822 AGENCOURT
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8	86	7.4	643	1	AL848045 AL848045
9	83.2	7.1	499	2	BF567596 BF567596
10	76	6.5	921	9	CNS03296 CNS03296
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19	73.8	6.3	830	2	BP315022 BP315022
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28	73.4	6.3	1081	4	BM805611 AGENCOURT
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37	71.2	6.1	1773	9	AY400782 Homo sapi
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BX643713  
ACCESSION DKFZP781C0629.5, mRNA sequence.  
VERSION BX643713  
KEYWORDS BX643713.1 GI:34478046  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 839)  
REFERENCE  
AUTHORS Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Oanger, A.,  
Fobo, G., Han, M. and Wiemann, S.  
TITLE Est (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS

MIPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden/Germany) within the CDNA sequencing  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZP781C0629) is available at the RZPD in Berlin.  
Please contact the RZPD: Resourcenzentrum, Heuberg 6, 14059  
Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.

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source location/Qualifiers

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#### ORIGIN

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Matches 546; Conservative 0; Mismatches 187; Indels 4; Gaps 1;  
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Db	166	TAGTAGCTTTTGGCTTAAATGCTAGAGAAATGCTTTGGTCAATTTAGCTTTTGTGGGACA	225
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Db	226	AAACCTTAGACATGGAATGATTTATTTTCTTAACTGAGCCATCTGACCTTCTTG	285
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Oy	248	AGCAAGCTTGCTATTTTGGCTCATCTACTGACTATCTTTATGTAACACATCTGCTATA	307
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VERSION	CF147821		
KEYWORDS	CF147821.1 GI:33244089		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (Bae 1 to 704)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/.		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Daniela S. Gerhard, Ph.D.		
	Office of Cancer Genomics		
	National Cancer Institute / NIH		
	Bldg. 31 Rm10A07 Bethesda, MD 20892		
	Email: cgapbs-r@mail.nih.gov		

Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
Plate: IRB102 row: b column: 07  
High quality sequence stop: 685.  
location/Qualifiers  
1. .704

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## ORIGIN

Query Match	35.1%	Score 410.6	DB 7	Length 704
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LOCUS				
DEFINITION				
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		IMAGE:738774 5', mRNA sequence.		
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VERSION		COSY9034.1	GI:51323616	
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SOURCE		Homo sapiens (human)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		1 (bases 1 to 721)		
AUTHORS		NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL		Unpublished (1999)		
COMMENT		Contact: Daniela S. Gerhard, Ph.D.		

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DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINTL at:  
<http://image.llnl.gov>  
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FEATURES	Location/Qualifiers
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from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
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**ORIGIN**

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Db	332	AGATTGTCTCATAGCTATGATATAAATACCTGTCAATCTCAAAATGCTTTGTCTTATGGA	391
Qy	368	CTCAGCACTCTGCGCACTCGAATAATGTACTC	400
Db	392	CGCAAAAAACGGGGGGCTGTAAAGAGGGAGACGC	424

RESULT 4	CD326085	853 bp	mRNA	linear	EST-28-MAY-2003
LOCUS	CD326085				
DEFINITION	AGAGCCOURT_14163426 NICHD_XGC_Eyel1 <i>Xenopus laevis</i> cDNA clone IMAGE:6949081 5', mRNA sequence.				
ACCESSION	CD326085				
VERSION	CD326085.1	GI:31090416			
KEYWORDS	EST.				
SOURCE	<i>Xenopus laevis</i> (African clawed frog)				
ORGANISM	<i>Xenopus laevis</i>				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 853)	NIH-MGC	<a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Daniela S. Gerhard, Ph.D.			

Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20895

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement:  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LHAM14564 row: F column: 24  
High quality sequence set: 707.

**FEATURES**  
**SOURCE**

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/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6949081"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NICHD XGC_Eyel"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; cloned unidirectionally. Primer: oligo dT Average insert size 2.3 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection XGC library."

```

**ORIGIN**

Query Match	10.9%	Score 127.8;	DB 6;	Length 853;
Best Local Similarity	58.6%	Pred. No. 2.9e-24;		
Matches 241; Conservative	0;	Mismatches 167;	Indels 3;	Gaps 1;

50 TGACATTTTAA TGTCTTACTAGCTATTGCTATTAATGTTAGGCAATGTCGTGTCATTT 109

Db 389 TGGCTGCTGATGAGGGGCTCTCATAGTGAACCGCTGGGGAATGCCGTGATGC 448  
 Qy 110 TAGCTTTATTTGTGGACAGAAATCTTACATCGAAGTAATTTCTTTCTTAACCTGG 169  
 Db 449 TGGCTTTGTTGTGGACCTCCGACCTCCGACCAATATTTCTTTCTTCTTCAACCTGG 508  
 Qy 170 CCATTCAGACTCTTTTGTGGGTGCAATTCGATCTCTGTACATACCTTCCTGCTGA 229  
 Db 509 CTATCTCAGATTTCTTTGTAGGTGCCCTGTGCATCCCTGTATGTGCAATGACGACTGA 568  
 Qy 230 CTTCAC---TGACCTCTGGAAGCAAGCTGTGTATTTTGGCTCACTTACGACTCTTT 286  
 Db 569 CTGGGAGATGAGCTTTGGCAGAGAGCGTTTGCAGACGCTGTCTGTGATTTATTCGC 628  
 Qy 287 TATGTACAGACTCTGTGTATATATTTGCTCATAGCTACAGATCGTACAGCTGACT 346  
 Db 629 TCTGACCTCTGCTGCTGTTCATCATCTGCTCATAGCTACAGAGTTCACTCTGTGA 688  
 Qy 347 CAATGCCGTGTGTATAGCTCAGCACTGTGCACTGTGAAAATGCTACTAGATGG 406  
 Db 689 CCGGGCTGTGACGTTACGAGCTCAGAGATGACAGCGCGCATGCTTGAATAATGA 748  
 Qy 407 TGGCTGTTGATTTCTCTTCATGACAAATGGCCGATGATTTCTGATTT 457  
 Db 749 CCATGCTGTGATCTTGGCTTTCTCTATATGACACGACCAATATATAT 799

RESULT 5  
 CB556920 672 bp mRNA linear EST 02-APR-2003  
 LOCUS AMGNND:UMGP1-00001-D6-A urgpl (14349) Rattus norvegicus cDNA clone  
 DEFINITION urgpl-00001-d6 5', mRNA sequence.

ACCESSION CB556920  
 VERSION CB556920.1 GI:29496320  
 KEYWORDS EST  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 672)  
 AUTHORS Amgen EST Program.  
 TITLE Amgen Rat EST Program  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Dan Fitzpatrick  
 Amgen, Inc  
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Fax: 805 447-4881  
 Place: 00001 row: d column: 6.

FEATURES  
 source Location/Qualifiers  
 1..672  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone\_lib="urgpl-00001-d6"  
 /note="Vector: pSPORT1; Rat GPCR library rearrayed  
 internal pSPORT vector."

## ORIGIN

Query Match 9.6%; Score 112; DB 6; Length 672;  
 Best Local Similarity 56.4%; Pred. No. 7.5e-20;  
 Matches 230; Conservative 0; Mismatches 175; Indels 3; Gaps 1;

Qy 59 TAATGCTTTACTAGCTATGCTATTAATTTAGGCAATGCTGTCATTTAGCTTTTA 118  
 Db 227 TCATGGCGTGTCTCATCGTGGCCACAGTACTGGGCAACGCGTGTGTCATGCTGCGCTTCG 296  
 Qy 119 TTGTGGACAGAAATCTTACATCGAAGTAATTTCTTTCTTAACCTGGCATTCGAG 178  
 Db 297 TGGCGATTCGAGCTCCGACCCAGAGAACACTCTTTTGTGTCACCTGCGCATCTCGG 356  
 Qy 179 ACTTCTTTGTGGGTGCAATTCCTCTGTATACATACCTTCTGCTGACTTAC---T 235

Db 357 ACTTCCTGTGGGGGCTTCTGCAATCCATGTAGTACCCATGTGCTGACCGGCCCT 416  
 Qy 236 GGACTTCGGAAGCAAGCTTGTGATTTTGGCTCATCTAGCTATCTTTATGATAG 295  
 Db 417 GGACTTCGCGCGGGGCTCTGCAAGCTGTGGGTGTGATCTACTTACTGTGCTCT 476  
 Qy 296 CATCTGTATTAATTAATGCTCTCATAGCTTACAGATCGTACAGTCAATGCGC 355  
 Db 477 CCGGCTCTTCAACATGTAATCTCATAGCTTACAGCCGATTCCTGTCACTGAGCTG 536  
 Qy 356 TGTGATAGAGCTCAGACTCTGCACTGCACTGCAAAATGCTACTAGATGCTGCTTT 415  
 Db 537 TCTCTTACAGGGCCACAGAGGGGACAGACGAGCCGCTTGGAGATGACACTGTGT 596  
 Qy 416 GGATATTCCTCTCATGCAATAGGCGCGATGATTTCTGATTTCAAGT 463  
 Db 597 GGTGCTGCTTCTCTGCTGTATGGGCTGCACTCTAGTTGGAGT 644

RESULT 6  
 CF147822 732 bp mRNA linear EST 25-JUL-2003  
 LOCUS AGNCOURT.14740187 NIH\_MGC.145 Homo sapiens cDNA clone  
 DEFINITION IMAGE:6971899 5', mRNA sequence.

ACCESSION CF147822  
 VERSION CF147822.1 GI:33244090  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 732)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE NIH-MGC  
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
 COMMENT Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: ggarbs-remail.nih.gov  
 Tissue Procurement: GPCR Consortium  
 cDNA Library Preparation: GPCR Consortium  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
 http://image.llnl.gov  
 Plate: IRB102 row: b column: 06  
 High quality sequence stop: 610.

FEATURES  
 source Location/Qualifiers  
 1..732  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:6971899"  
 /tissue\_type="mixed"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC 145"  
 /note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
 varies by clone; ORFs were PCR-amplified and cloned into  
 pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
 clone and include the following: 5'-EcoRV-XbaI/XhoI-3',  
 5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).  
 For information about which gene each clone represents,  
 please visit our anonymous ftp site at  
 ftp://image.llnl.gov/image/rearrayed\_plates/IRB1.presv.dat  
 a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 9.3%; Score 109.2; DB 7; Length 732;  
 Best Local Similarity 52.7%; Pred. No. 4.7e-19;  
 Matches 293; Conservative 0; Mismatches 248; Indels 15; Gaps 2;

Oy		59	TAAATGCTTTACTAGCTATTGTGTAATAAGTAAAGCAAGAATGGTGTCATTTTAGCTTTA	118
Db		135	TCAATGGCGCCTCTCATCTGTGCACAGGTGTGGGACAAGCCGTGTCTATGCTCGCTTCC	194
Oy		119	TTGTGACACAGAAATCTTAGACATGCAAGTAATTACTTTTTTTCTTAACCTTGGCCATTG	178
Db		195	TGGCCGACTCGAGCCTCCGCCAACCCGAACAACCTTCTCTGCTCAACCTCGGCATCTCCG	254
Oy		179	ACTTCTTTTGGGGTGGCAATTGCAATTCTCTGTACATACCTTCTCGCTGAC---TACT	235
Db		255	ACTTCTCTGTGGGGCCTTTCGATCCCACTGTATGTACCCTTACCTGTGTGACAGGCCCT	314
Oy		236	GGACTTTCGGAAGCAAGCTGTGTGATTTTGGCTCATTAAGCTATGCTATCTTTTATGTAC	295
Db		315	GGACCTTCGCGCGGGGCTCTGCAAGCTGTGTGCTGTGTGTGTGACCTACTGCTGTACCT	374
Oy		296	CATCTGTGTATTAATATTGTCTCTCATTCAGCTACAGATCGCTACAGTCTTCAAATGCG	355
Db		375	CCTCTGCTTCAACATCGTGTCTCATTCAGCTACGACCGGCTCTGTGCGATCACCGAGGG	434
Oy		356	TGTGTATAGAGCTTCAGCACTCTGGCACCTGTGAAAATTGTCTACATCAATGTGTGCTG	415
Db		435	TCTATATACCGGGCCACGACGGGTATCAACGCGCGGAGTCGGAAGATGTGCTGTGTGT	494
Oy		416	GGATATTTCTCTTCATATGACAATATGGGCGGATGATCTGTATTTACAGCTTTGGCAGATA	475
Db		495	GGGTGTGTGGCTTCTCTGTGTATCGGACCAAGCATCTGTAGCTGGGAGTAACTGTCCGGG	554
Oy		476	GCACCTAC-----AGAAATGTGAACCTGTGATTTTAAAAAAGTGTACTTTGCTC	523
Db		555	GCACCTCCATCCCCGAGGGCCACGTGCTATGCGCAGTTCTTCAACAATGTACTTTCTTCA	614
Oy		524	TCCCTACATCATTAATTGGAATTTCCGATCCCCATCTTGTAGTGTCTATTTCAGCGCC	583
Db		615	TCAGGCGCTTCAACTGTGAGTTCTTTACGCCCTTTCAGGCGTCACTTCTTTTAACCTCA	674
Oy		584	ATATTACTGAGAGCCT	599
Db		675	CCATCTACCTGACAT	690
RESULT 7				
LOCUS		CC481311	684 bp	DNA linear GSS 16-JUN-2003
DEFINITION		CH240_309C10_T7 CHORI-240 Bos taurus genomic clone CH240_309C10,		
ACCESSION		CC481311		
VERSION		CC481311.1		
KEYWORDS		GSS.		
SOURCE		Bos taurus (cow)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
		Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
		Bovinae; Bos.		
REFERENCE		1 (bases 1 to 684)		
AUTHORS		Holt,R., Stott,J., Yang,G., Barber,S., Smallus,D., Prabhu,A.-L.,		
		Tait,M., Cloutier,A., Lee,D., Guin,N., Olson,T., Mayo,M.,		
		Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,		
		Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,		
		Schein,J.J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,		
		Daylampe,B.P. and Tellam,R.		
		Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398		
		Unpublished (2003)		
TITLE		Other GSSs: CH240_309C10.TARBAIC1P2		
JOURNAL		Contact: Rob Holt		
COMMENT		Sequencing		
		The British Columbia Cancer Agency Genome Science Centre		
		600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6		
		Tel.: 604-877-6065		
		Fax: 604-877-6276		
		Email: rholt@cgsc.ca		
		Clones are derived from the bovine BAC library CHORI-240		

(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong ([pdjong@chori.org](mailto:pdjong@chori.org)). Clones may be purchased from BACPAC Resources ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.

Plate: 309 row: C column: 10

Seq primer: T7

Class: BAC ends.

FEATURES	source	location/Qualifiers
		1..684
		/organism="Bos taurus"
		/mol_type="genomic DNA"
		/strain="bred: Hereford"
		/db_xref="taxon:9913"
		/clone="CH240_309C10"
		/sex="Male"
		/cell_type="Blood"
		/clone_lib="CHORI-240"
		/note="Vector: pTARBAC1.3, Site_1: MboI, Site_2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"
ORIGIN		
Query Match	8.9%; Score 104.4; DB 9; Length 684;	
Best Local Similarity	67.4%; Pred. No. 1e-17;	
Matches	147; Conservative 0; Mismatches 71; Indels 0; Gaps 0;	
QY	147 TAATTACTTTTCTTTTAACCTGGCATTGCGAGCTCTTTGGTGTCGAATTGCAATTCC	206
DB	260 TACGGCTAATATTTGTTAATCTTAATTTTTCGCCCAATGACAGTATGATCTTCATTTCC	319
QY	207 TCTGTACATACCTTCTCGCTGACTTACTGTGACTTCTGAAAGCAAGCTGTGTATTTTG	266
DB	320 TTATTTATCCTCCCTCAAGCTCTTCACTGSGAATTTGAAATAACATTTGTGCTTTTG	379
QY	267 GCTCATTAAGTACTATCTTTTATGTAAGCATCTGTGTATATATTTGCTCTCATGCTTA	326
DB	380 GCTCACTACAGTACTATCTTTTGTGTAAAGCATCTGTGTATATACATCGTACTCATGCTT	439
QY	327 CGATCGCTACAGTCAAGCTTCAATGCGGTGTATTA 364	
DB	440 TGATCGATATCAGTCAGTCTTCAATGCTGTATGATCAAA 477	
RESULT 8		
ALB48045		
LOCUS		
DEFINITION	ALB48045 XGC-egg Xenopus tropicalis cDNA clone TGG9022122 5', mRNA	643 bp mRNA linear EST 26-NOV-2003
ACCESSION	ALB48045	
VERSION	ALB48045.2	GI:38559584
KEYWORDS		EST.
SOURCE		Xenopus tropicalis (western clawed frog)
ORGANISM		Xenopus tropicalis
		Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE		1 (bases 1 to 643)
AUTHORS		Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE		Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL		Unpublished (2003)
COMMENT		On Sep 15, 2002 this sequence version replaced gi:22868310.
		Contact: Taylor R
		Sanger Institute
		Hinxton, Cambridgeshire, CB10 1SA, UK
		Email: <a href="mailto:tropesanger.ac.uk">tropesanger.ac.uk</a>
		Sanger Xenopus tropicalis EST project 2001
		TROPICALIS_SEQUENCE_ID: TGG9022122.plkSP6
		Sequencing primer: SP6
		This sequence is from a Xenopus Gene Collection (XGC) library
		constructed by Aaron W. Zorn.

cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.  
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the  
5' end and NotI at the 3' end.  
Vector: pCS107; Site 1: EcoRI; Site 2: NotI  
Host: Escherichia coli XL1-blue.  
Location/Qualifiers

FEATURES  
source

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1..643
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/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="EB9022122"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_1ib="XGc-egg"
/notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
```

## ORIGIN

Query Match 7.4%; Score 86; DB 1; Length 643;

Best Local Similarity 53.1%; Pred. No. 1.5e-12;  
Matches 238; Conservative 0; Mismatches 195; Indels 15; Gaps 2;

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190 GGTGAATTGCAATTCCTCTGTACATCCTTCTGCTGACT--TACTGACTTTCTGGA 246
|||||
83 GGTGATTCGTGATCCCACTCTATATCCCTTATGCTGACGCGCAGTGAAGTTGGG 142
|||||
247 AAGCAAGCTGTGTATTTGGCTCATTTACTGATCTTTTATGTACAGCATCTGTAT 306
|||||
143 AAAGCTGTGCAAGTGTGCTAGTAAGACTACCTTTATGACACTGCTTCAGCTTTT 202
|||||
307 AATATTGCTCATGAGTACGATCGCTACGCTCAAGTCTCAATGCGGTGATAGA 366
|||||
203 AATATTGCTCATGAGTACGATCGCTACGCTCAAGTCTCAATGCGGTGATAGA 262
|||||
367 GCTCAGACTGTGCACTGTGAAATTTGCTACTCAGATGCTGCTTTTGAATTTCTC 426
|||||
263 GCACAGAAAGAAATGACAAAGAAATGACAGTGTAAATGCTTATGTTGGTGACAGC 322
|||||
427 TTCAATGACAAATGCGCCGATGATTTCTGATTTCAAGACTCTTGCGAATATGACTA 481
|||||
333 TTCTTCTCTAAGCCCAAGCATCACTCTGGAATATGCAAGAACTACTATCTTA 382
|||||
482 -----CAGATGTGAACCTGATTTTAAAGATGCTTGTGCTCTCCCTACATCA 534
|||||
383 CCAGAAAGGAGATGTATGTATGATTAATTTCTAATCAATGCTATTTCTGATGATCTTC 442
|||||
535 TTATTGGAATTCCTGATCCCATCTTTGTTGATTTGCTTATTTGAGGCCCAATTTACTGG 594
|||||
443 ACAATAGAAATCTTATCTCATTTCAATCAGTGTACTTCAATCTAAGCATCTACATT 502
|||||
595 AGCCTGTGGAAGCGAGAAACTGAGCA 622
|||||
503 AACATCAAAAGGAACTATGATGAGAA 530
```

## RESULT 9

BF567596

LOCUS BF567596 499 bp mRNA linear EST 12-DEC-2000  
DEFINITION UI-R-B00-agr-c-06-0-UI.r1 UI-R-B00 Rattus norvegicus cDNA clone  
UI-R-B00-agr-c-06-0-UI 5', mRNA sequence.

## ACCESSION

BF567596

## VERSION

BF567596.1 GI:11677326

## KEYWORDS

EST

## SOURCE

Rattus norvegicus (Norway rat)

## ORGANISM

Rattus norvegicus

## REFERENCE

1 (bases 1 to 499)

## AUTHORS

Bonaldi,M.F., Lennon,G. and Soares,M.B.

## TITLE

Normalization and subtraction: two approaches to facilitate gene

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

discovery  
Genome Res. 6 (9), 791-806 (1996)  
9704447  
8889548  
Contract: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
clones will be available through Research Genetics (www.resgen.com)  
This clone is also available through the I.M.A.G.E. Consortium at  
ILNLI (info@image.llnl.gov). IMAGE ID= 1796445  
Seq primer: M13 Forward  
Location/Qualifiers

FEATURES  
source

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1..499
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B00-agr-c-06-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_1ib="UI-R-B00"
/notes="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The library
(UI-R-B00) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratatc.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldi, Lennon and Soares, Genome Research
6:791-806, 1996)"
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## ORIGIN

Query Match 7.1%; Score 83.2; DB 2; Length 499;

Best Local Similarity 53.1%; Pred. No. 8.3e-12;  
Matches 231; Conservative 0; Mismatches 189; Indels 15; Gaps 2;

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189 GGTGCAATTCATTCCTCTGTACATCCTTCTGCTGACTTAC--TGGACTTCTGG 245
|||||
58 GGGTCCCTTGCAATCCATGATGATGATGATGATGATGATGATGATGATGATGAT 117
|||||
246 AAAGCAAGCTGTGATTTGGCTCATTTACTGACTATCTTTTATGTACAGACTCTGTGA 305
|||||
118 CCGGGGCTCTGCAAGCTGTGCTGTGTGTAGACTTACTGTGTGCTCTCTCGTCTT 177
|||||
306 TAAATTTGCTCATGAGTACGATTCGCTACAGTACGATTCGAATGCGGTGATATG 365
|||||
178 CAACATCTACTCATGAGTATGACCGATTTCTGTGATCTACGAGCTGTCTCTACAG 237
|||||
366 AGCTCAGACTCTGGCACTGGAATATGCTACTCAGATGTGTGCTGTGATATTTCTC 425
|||||
238 GGGCCAGAGGGGGGACAGAACGGCGCTTCCGAAAGTGAAGTGTGTGTGCTGTGCT 297
|||||
426 CTTATGCAAAATGGCGCGATGATTTGATTTTCAAGCTCTTGGCAATATGACTAC-- 482
|||||
298 CTTCTGCTGTATGGGCTGTGCATCTGAGTTGGGAGTACCTGTCTGTGAGAGTTCAAT 357
|||||
483 -----AAGATGTGAACCTGATTTTAAAGATGCTTGTGCTCTCCCAATC 533
|||||
358 CCGGAGGCGCACTGTCTGTGATTTCTTCACTGATGATTTTCAATCAAGCATCAGACT 417
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534 ATTATGGAATTCCTGATCCCATCTTGTATGTTGCTTATTTCAAGCGCCATATTTACTG 593
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418 CACCTCGAGTTTCTTCAAGCGCTTCTCAGGTTACCTTTTCAACCTCAGATCTTACT 477
|||||
594 GAGCTGTGGAAGCG 608
|||||
```

Db	478	GAACATCCAGAGGCG	492
RESULT 10	CNS03296	921 bp	DNA
CNS03296/c			Linear
LOCUS			SS 01-SEP-2000
DEFINITION	Tetradon nigroviridis genome survey sequence T7 end of clone 206D09 of library G from Tetradon nigroviridis, genomic survey sequence.		
ACCESSION	AL224547.1	GI:7883412	
VERSION	AL224547		
KEYWORDS	SS; genome survey sequence.		
SOURCE	Tetradon nigroviridis		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Telostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.		
REFERENCE	1		
AUTHORS	Roest Crollius,H., Jailon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzames,C., Wincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.		
TITLE	Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
PUBMED	10835645		
REFERENCE	2		
AUTHORS	Roest Crollius,H., Jailon,O., Dasilva,C., Ozouf-Costaz,C., Fitzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.		
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis		
JOURNAL	Genome Res. 10 (7), 939-949 (2000)		
MEDLINE	20359837		
PUBMED	10899143		
REFERENCE	3 (bases 1 to 921)		
AUTHORS	Genoscope.		
TITLE	Direct Submision		
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequence :		
COMMENT	BP 191 9106 EVRY cedex - FRACB (E-mail : seqref@genoscope.cns.fr Web : www.genoscope.cns.fr) This sequence is a single read and was generated as part of a large scale clone-and sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetradon">http://www.genoscope.cns.fr/Tetradon</a> .		
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	/note="Genoscope sequence ID : C0AG206CB05L1-end : T7"		
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Query Match	6.5%;	Score 76;	DB 9;
Best Local Similarity	57.8%;	Pred. No. 1,1e-09;	
Matches 156;	Conservative 0;	Mismatches 110;	Indels 4;
		Gaps 1;	
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Db	588	CTGTTCAGAGCAAAAAGATTGCCAAATCTCTGGCCATTATCGTGTATTTTCGGATC	529
Db	943	TGCTGGGCTCATATCTGACTCACTATCTATCTCATTTTTCCTGAAAGAACTTG	1002
Db	528	TGCTGGGCCCCCTACACGCTGTGATGATCATCTCGCGCGCTGCAGCGCAGTGGCGTG	469
Db	1003	ACTAATCAACCTGTATCACTACTCTCTTTGGCTCCAGTGGTTCATTTCTTTTAT	1062
Db	468	CGAGTA-----CTGTTCAGAGTAATCTTTGGCTCTGTGGCTCAACTCAGCATCAAC	413
Db	1063	CCCTTTTGTATCATGTGTTCACAAAGCTTTTCAGAAAGCTTTTCGAAAAATCTTCT	1122

Db	LOCUS	RESULT 11
0y	1123 GTGAGAGGCAATCCAGCAGCACACACAC 1152	
Db	352 CCCAAAAGACAGTGGCTTCCAGCCTCATG 323	
REFERENCE	BY728212 663 bp mRNA linear EST 17-DEC-2002	
AUTHORS	BY728212 RIKEN full-length enriched, adult male corpus striatum Mus musculus cDNA clone C030026C2 5', mRNA sequence.	
VERSION	BY728212	
KEYWORDS	BY728212.1 GI:27141339	
SOURCE	EST.	
ORGANISM	Mus musculus (house mouse)	
	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
	1 (bases 1 to 663)	
	0kazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikiato,I., Oseato,N., Saito,R., Suzuki,H., Yamana,A., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Balderelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Brad,D., Brusci,V., Clotiaux,C., Corbani,L.E., Cousins,S., Dalla,E., Drganic,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Guclinich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawai,H., Kawasawa,Y., Kedzierzka,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramchandran,S., Rasmussen,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sanderlin,A., Schneider,C., Sample,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wallestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wysshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Cantinici,P., Hayatsu,N., Hirozane-Kienhaka,T., Komno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Aizawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Komno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,S., Numazaki,R., Onno,M., Ohata,N., Saito,R., Sakazume,N., Sano,H., Saeki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,W., Takeda,Y., Waki,K., Watanaki,A., Muramatsu,M. and Hayashizaki,Y.	
	Direct Submission	
	Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)	
	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new	
TITLE	CONTACT: Yoshihide Hayashizaki	
JOURNAL	Laboratory for Genome Exploration Research Group, RIKEN Genomic	
MEDLINE	Sciences Center (GSC), Yokohama Institute	
PUBMED	The Institute of Physical and Chemical Research (RIKEN)	
COMMENT	1-7-22 Stehro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan	
	Tel.: 81-45-503-9222	
	Fax: 81-45-503-9216	
	Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/	
	Adachi,J., Aizawa,K., Akimura,T., Aizawa,T., Caninici,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Komno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,S., Numazaki,R., Onno,M., Ohata,N., Saito,R., Sakazume,N., Sano,H., Saeki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,W., Takeda,Y., Waki,K., Watanaki,A., Muramatsu,M. and Hayashizaki,Y.	
	22354683	
	Nature 420, 563-573 (2002)	
	12466851	

Genes. Genome Res. 10 (10), 1617-1630 (2000).  
Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000).  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001).  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

**FEATURES**  
**SOURCE**

1. .663  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
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/note="Site\_1: Sali; Site\_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAAGACGATTCCTTTTCTTTTTTTTAA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGATTCTCGAGTAATAATTAATTAATCCCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PUC I. Cloning sites, 5' end: Sali; 3' end: BamHI."

**ORIGIN**

Query Match	6.5%	Score 75.6;	DB 6;	Length 663;
Best Local Similarity	54.2%;	Pred. No. 1.2e-09;		
Matches 175;	Conservative	0;	Mismatches 145;	Indels 3;
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Db 342 CAGAGCTCAAGACAGTCAACAACCTACTTCTCTGAGCCTGGCCGTGCTGATCTCATCA 401  
QY 188 TGGGTGCAATTGCAAATTCCTCTGTACATACTTCTCGCTGACTT--ACTGGACTTGTG 244  
Db 402 TTGGCACTTTCTCCATGAACCTCTTAACACATACCTGCTGATGGGCCACCTGGGCTCTGG 461  
QY 245 GAAGACAGCTTTGTGATTTTGGCTCATTAAGCTATCTTTTAATGTACAGACTGTGT 304  
Db 462 GCACACTGGGCTGTGACTCTGTGGCTGGCCCTTGAATTAATGTGCCAGCAAGCTCTGTCA 521  
QY 305 ATATAATTGCTCTCATCAGCTACGATCGCTACAGCTCAGTCTCAAAATGCCGTGTGATATA 364  
Db 522 TGAACTCTTGCTCAATCAGCTTGAACCGTTACTTCTAGTACCGAACCCCTGAGCTAAC 581  
QY 365 GAGCTCAGCACTTGGCACTGTG 387

Db 582 GAGCCAAGCGCACTCCCCGCGAGG 604

RESULT	12
LOCUS	CD804122
DEFINITION	CD804122 795 bp mRNA linear EST 15-JUL-2003
VERSION	UI-M-GVO-chu-g-19-0-UI.r1 NIH_BMAP_GVO Mus musculus cDNA clone
KEYWORDS	IMAGE:30545730 5', mRNA sequence.
SOURCE	CD804122 CD804122.1 GI:32462948
ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 795) NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.
JOURNAL	
COMMENT	

Tissue Procurement: Dr. Jim Lin University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mouse1.html>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
seq primer: pyx-5.

## FEATURES

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/note="Organ: Brain; Vector: pYX_Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX_Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGACGACGAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Heman Chin, Ph.D., program coordinator."

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## ORIGIN

Query Match	6.4%;	Score 75;	DB 6;	Length 795;
Best Local Similarity	54.2%;	Pred. No. 1.9e-09;		
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Oy	188	TGGGTGCAATTGCATTTCTCTGTACATACCTTCTCGAGACTT--ACTGGACTTCTG	244
Db	219	TTGGCACTTTCTCCATTAACCTCTATATGCAATATACCTGTATAGGACCACTGGGCTGG	278

QY	245	GAAGCAAGCTGTGTATTTTGGGCATTAACGACTATCTTTTAACTAGACATCTGTGT	304
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QY	305	ATAATATTTGCTCTCATCTAGTACGATCGCTACCAAGTCAATGCCGTGTGTATA	364
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QY	365	GAGCTCAGCACTCTGGCACCCTGG	387
Db	399	GAGCCAGACGCACTCCCGCAGG	421
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DEFINITION	603025570P1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5199905 5',	940 bp	mRNA linear EST 25-SEP-2001
ACCESSION	BI757352		
VERSION	BI757352.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 940)		
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 940)	NIH-MGC	<a href="http://mgc.ncbi.nlm.gov/">http://mgc.ncbi.nlm.gov/</a> .		
	National Institutes of Health,	Mammalian Gene Collection (MGC)		
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: <a href="mailto:cgabbe@omail.nih.gov">cgabbe@omail.nih.gov</a>			
	Tissue Procurement: Life Technologies, Inc.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNL at:			
	<a href="http://image.lnl.gov">http://image.lnl.gov</a>			
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	High quality sequence stop: 865.			

FEATURES	Location/Qualifiers
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/clone_1fb="NIH_MGC_114"
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**ORIGIN**

Query Match	6.4%	Score 75	DB 4	Length 940
Best Local Similarity	52.7%	Pred. No. 2e-09		
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Oy	128	GAAATCTTAGACATGGAAGTATTACTTTTTTTTAACTGGCCATTGACACTCTTTGG	187
Db	335	CGAGACTCAAGACACTCATATACTACTTCTGTGTAGCTGGCCCTGTGTGTACCTCAATCA	394
Oy	188	TGGGTGCAATTGCATTCTCTGTATCATACCTTCTCTGGTAGCTT--ACTGGACTTGTG	244

Db	395	TCGGTACTCTTCACATGAACCTGTATACAGTACACCTGCTCATAGGCGCACTGGGCTCTGG	454
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DEFINITION	Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone: C03026622 product:MOSCAINIC ACETYLCHOLINE RECEPTOR M1, full insert sequence.
ACCESSION	AK081248
VERSION	AK081248.1 GI:26349070
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

**TITLE** Itoh M., Komno H., Okazaki Y., Muramatsu M. and Hayashizaki Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
**JOURNAL** Genome Res. 10 (10), 1617-1630 (2000)  
**PUBMED** 20499374  
**PUBMED** 11042159

## AUTHORS

**AUTHORS**  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, T., Sasaki, N., Carinci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Suni, M., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamanoto, R., Matsumoto, H., Sekiguchi, S., Ikegami, T., Kashiwaagi, K.,  
Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kikara, T. and Hayashizaki, Y.  
**TITLE**  
RIKEN integrated sequence analysis (RISA) system—334-format  
sequencing pipeline with 384 multicapillary sequencer  
**JOURNAL**  
Genome Res. 10 (11), 1757-1771 (2000)  
**MEDLINE**  
20530913  
**PUBMED**  
11076681

## AUTHORS

TITLE	JOURNAL	REFERENCE
PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection	Nature 409, 685-690 (2001)	5

TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 3816)

**AUTHORS**  
Aachida, S., Aizawa, K., Akimura, T., Aikawa, T., Bono, H., Carnini, P.,  
Fukuda, S., Furuno, M., Hanaagaki, T., Hara, A., Hashizume, W.,  
Hayashi, K., Hayatsu N., Hiramoto, K., Hiraoka, T., Hirokawa, T.,  
Hori, F., Imocant, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,

**TITLE**  
**JOURNAL**

Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Satoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiroki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takekda, Y., Tanaka, T., Tomatsu, A., Toyota, T., Yasunishi, A., Murakatsu, M., and Hayashizaki, T.

**COMMENT**

Direct Submission  
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Sueniwa-cho, Tsurumi-ku, Yokohama  
Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp,  
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>.

**CDS**

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**ORIGIN**

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QY	282	TCTGTCTTCGCGCTACAGTACAGGCAACTGCTGTCTCATCTCTTCAGAGTCAACA	341
Db	128	GAATCTTAGACATCGAAGTAATTACTTTTCTTAACCTGGCCATTGSCAGACTCTTTG	187
QY	342	CAGAGCTCAGACAGTCAACAACTACTTCGTGTGAGCGCTGGCCGTGTGTATCTACACA	401
Db	188	TGGGTGC AATGCGAATTCCTCTGTACATACTTCTCGCTGACTT--ACTGGACTTCG	244
QY	402	TTGGCACTTCTTCATGAACCTCTATACCAATATCTTCTCATATGGGCCACTGGGCTCTGG	461
Db	245	GAAGCAAGCTTGATATTTTGGCTCATTAACGACTATCTTTATATGACAGCATCTGAT	304
QY	462	GCAACATCGCCTGTGACCTCTGGCTGGCGCTGGACTATGTGGCCAGCAACGCTCTTGCA	521

## ORGANIS

## REFERENCE

AUTHORS  
TITLE

## JOURNAL

COMMENT:

Food and Feed Safety Research Unit  
USDA/ARS, Southern Regional Research Center  
1100 Robert E. Lee Boulevard, New Orleans, LA 70124, USA  
Tel: 504 286 4405  
Fax: 504 286 4419  
Email: [jjuny@errc.ars.usda.gov](mailto:jjuny@errc.ars.usda.gov)  
Contact Dr. Yu at [USDA/ARS SRRC \(jjuny@errc.ars.usda.gov\)](mailto:USDA/ARS SRRC (jjuny@errc.ars.usda.gov)) for clone  
information  
PCR Primers  
FORWARD: M13F  
BACKWARD: M13R  
Seq primer: M13 Forward  
POLYA=No.

## FEATURES

**source**

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/organism="Aspergillus flavus"
/mol_type="mRNA"
/strain="NRRL 3357"
/db_xref="taxon:5059"
/clone="NAFC784"
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/cell_type="mycelia"
/dev_stage="developmental stages from 18 to 96 hours"
/lab_host="E. coli DH10 T1 resistant cells"
/clone_lib="Aspergillus flavus Normalized cDNA Expression library"
/note="Vector: pBluescript (SK+) (Stratagene), antibiotic selection marker: Carbenicillin; Site 1: NotI, at the 5 prime end; Site 2: EcoRI, at the 3 prime end; This normalized cDNA expression library was constructed using mixture of mycelial cells grown under eight different medium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off before ligating to vector."

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**ORIGIN**

Query Match 6.4%; Score 74.8; DB 7; length 700;  
 Best Local Similarity 60.1%; Pred. No. 2.1e-09;  
 Matches 143; Conservative 0; Mismatches 92; Indels 3; Gaps 1

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D5  
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Db 275 GTGTCATTCAGTTCCTATCAAAATTAACCTTTGGCTTTGGATCAATTCCTCTGA 334
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Search completed: August 5, 2005, 20:15:13  
 Job time : 3589 secs

Page Mark (1804)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 01:48:33 ; Search time 159 Seconds  
(without alignments)  
953.192 Million cell updates/sec

Title: US-10-626-398-10  
Perfect score: 2036  
Sequence: 1 MLANNSTIALTSIKISLFTL.....LKILPVROSTPPHNRISST 389

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	2036	100.0	389	US-10-626-126-10
3	2036	100.0	389	US-10-626-398-10
4	1308.5	64.3	390	US-09-812-216-2
5	1308.5	64.3	390	US-09-910-411-2
6	1308.5	64.3	390	US-09-875-076-14
7	1308.5	64.3	390	US-09-876-252-14
8	1308.5	64.3	390	US-09-852-165-2
9	1308.5	64.3	390	US-09-891-138A-6
10	1308.5	64.3	390	US-10-052-193-2
11	1308.5	64.3	390	US-10-225-567A-629

12	1308.5	64.3	390	US-10-272-983-14	Sequence 14, Appl
13	1308.5	64.3	390	US-10-354-769-2	Sequence 2, Appl
14	1308.5	64.3	390	US-10-393-807-14	Sequence 14, Appl
15	1308.5	64.3	390	US-10-417-820A-14	Sequence 14, Appl
16	1308.5	64.3	390	US-10-349-253A-2	Sequence 2, Appl
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18	1308.5	64.3	390	US-10-723-955-14	Sequence 14, Appl
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20	1308.5	64.3	390	US-10-737-619-2	Sequence 2, Appl
21	1308.5	64.3	390	US-10-626-445-2	Sequence 2, Appl
22	1308.5	64.3	390	US-10-684-206-20	Sequence 20, Appl
23	1308.5	64.3	390	US-10-616-088-2	Sequence 2, Appl
24	1308.5	64.3	390	US-10-626-126-2	Sequence 2, Appl
25	1308.5	64.3	390	US-10-626-398-2	Sequence 2, Appl
26	1306.5	64.2	390	US-10-290-078-27	Sequence 27, Appl
27	1237	60.8	391	US-10-626-445-8	Sequence 8, Appl
28	1237	60.8	391	US-10-626-126-8	Sequence 8, Appl
29	1237	60.8	391	US-10-626-398-8	Sequence 8, Appl
30	1236.5	60.7	391	US-10-626-445-9	Sequence 9, Appl
31	1236.5	60.7	391	US-10-626-126-9	Sequence 9, Appl
32	1236.5	60.7	391	US-10-626-398-9	Sequence 9, Appl
33	694.5	34.1	413	US-09-891-053-1	Sequence 1, Appl
34	694.5	34.1	413	US-10-759-463-1	Sequence 1, Appl
35	689.5	33.9	445	US-09-350-206-2	Sequence 2, Appl
36	689.5	33.9	445	US-09-349-755-2	Sequence 2, Appl
37	689.5	33.9	445	US-09-166-334-2	Sequence 2, Appl
38	689.5	33.9	445	US-10-282-958-2	Sequence 2, Appl
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40	689.5	33.9	445	US-10-453-106-1	Sequence 1, Appl
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42	689.5	33.9	445	US-10-757-263-132	Sequence 132, App
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44	689.5	33.9	453	US-09-891-053-20	Sequence 20, Appl
45	689.5	33.9	453	US-10-759-463-20	Sequence 20, Appl

#### ALIGNMENTS

RESULT 1  
US-10-626-445-10  
; Sequence 10, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 389  
; TYPE: PRT  
; ORGANISM: Cavia porcellus  
; US-10-626-445-10

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## RESULT 2

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; Sequence 10, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-10-626-126-10
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## RESULT 3

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; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-10-626-398-10
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Query Match 100.0%; Score 2036; DB 17; Length 389;
Best Local Similarity 100.0%; Pred. No. 7.1e-170; Indels 0; Gaps 0;
Matches 389; Conservative 0; Mismatches 0;
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Db 1 MLANNSTIALTSIKISLTFELMSLAIAMLGNNVVIAPFIVDRNLRHRSNYFFNLAIAD 60
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; Publication No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
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/ TITLE OF INVENTION: Histamine receptor
/ FILE REFERENCE: CN01069
/ CURRENT APPLICATION NUMBER: US/09/812,216
/ CURRENT FILING DATE: 2001-03-19
/ PRIOR APPLICATION NUMBER: 09/414,010
/ PRIOR FILING DATE: 1999-10-07
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patent Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 390
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-812-216-2
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RESULT 5
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/ Sequence 2, Application US/09910411
/ Patent No. US20020137054A1
/ GENERAL INFORMATION:
/ APPLICANT: Bergema, Derek
/ APPLICANT: Fitzgerald, Laura
/ APPLICANT: Li, Xiaolong
/ APPLICANT: Michalovich, David
/ TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
/ FILE REFERENCE: GP70655-2C1
/ CURRENT APPLICATION NUMBER: US/09/910,411
/ CURRENT FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: 09/693,761
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 09/497,790
/ PRIOR FILING DATE: 2000-02-03
/ PRIOR APPLICATION NUMBER: 09/431,898
/ PRIOR FILING DATE: 1999-11-02
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 390
/ TYPE: PRT
/ ORGANISM: Homo sapien
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US-09-910-411-2

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Query Match 64.3%; Score 1308.5; DB 9; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFELMSLAIAMGNVVLAFIVDRNLHRSNYFELNLAIDFV 63
DB 5 NSTINSLSTRVTLAFNFMGLVAFALMGNALVILAFVDRNLHRSSYFELNLAIDFV 64
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DB 125 QHTGVAKITVLAAVAVLAFVAVGPMILVSESKWDGSECEPGEFSEWYTLAITSLEFLV 184
QY 184 IPIILVAFSAHIYMSLMKREKLSRCLSHFVLPSDSSSDHGHSCQDPPSRATLPARKE 243
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RESULT 6
US-09-875-076-14
/ Sequence 14, Application US/09875076
/ Publication No. US20030017528A1
/ GENERAL INFORMATION:
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
/ FILE REFERENCE: AREN0050
/ CURRENT APPLICATION NUMBER: US/09/875,076
/ CURRENT FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 09/417,044
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/156,653
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PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,633  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,555  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,634  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/157,280  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,294  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,281  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,293  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,282  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 390  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-875-076-14

Query Match 64.3%; Score 1308.5; DB 10; Length 390;  
Best Local Similarity 65.1%; Pred. No. 4.3e-106;  
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

5 NSTIALT-SIKISLTFLNLSLAIATMGVVTIAFIVDRNRHRSNRYFNLATADFFV 63  
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
5 NSTINLSSTRVTALFFMSVLVAFALMGVALVILAFVVDKNRHRSSYFFNLATSDFFV 64  
64 GAIAIPLYPSGLTWTSGKQACVFLINDYLLCTASVNIYLISDRQVSNVWVRA 123  
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
65 GVISIPLYPHLTFEFDKGEICVFMILTDTYLLCTASVNIYLISDRYLSNVAVSRT 124  
124 OHSGTWKATQWVAWVIFSFMTNGPMILISDSMONSTTECEBGLKKWYFALPTSLBEL 183  
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
125 QHTGVLTITLWVAVVLAFLVNGPMILIVSESKDGECSCEGFSEWYILATISLELV 184  
184 IPIILVAYSANITWYSLMKREKLSRLSHPVLPSSSSSDHGHSCRPDPSATTPARKE 243  
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
185 IPIILVAYNNINIWYSLMKRDHLSRQSHPGTLA-VSSNICGHSFGRSLSSRSASTE 243  
244 TTASIGSDSRKRSLSLPSIRAYKSNVYASKMGFLSHSDSLALQOREHIEFPAKRLAK 303  
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
244 VPSHFSERQKRKSSLMFSRTRKNSNTIASKMGFSOSDSVALHOREVELLRARLAK 303  
304 SLATILAAFAICWAPYSLTTVIYSPPERNLTGSTWYHTAFWLQWFNSFVNPLYPLCHK 363  
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304 SLATILGVAVCWAPYSLFTIYVFSYASATGPKSVYRIAPWLQWFNSFVNPLYPLCHK 363  
364 RFOKAFKLTPVRQSTP-PHNRISIT 389  
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364 RFOKAFKLKICIKOPLPSQHSRSVS 390

RESULT 7  
US-09-876-252-14  
Sequence 14, Application US/09876252  
Publication No. US20030018182A1  
GENERAL INFORMATION:  
APPLICANT: Behan, Dominic P.  
APPLICANT: Lehmann-Brinlenc, Karin  
APPLICANT: Chalmers, Derek T.  
APPLICANT: Lowitz, Kevin P.  
APPLICANT: Lin, I-Lin  
APPLICANT: Dang, Huong T.  
APPLICANT: Chen, Ruoping  
APPLICANT: Liaw, Chen W.  
TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Rec  
FILE REFERENCE: AREN-0054

CURRENT APPLICATION NUMBER: US/09/876,252  
CURRENT FILING DATE: 2001-06-07  
PRIOR APPLICATION NUMBER: 09/416,760  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: 09/170,496  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: 60/110,060  
PRIOR FILING DATE: 1998-11-27  
PRIOR APPLICATION NUMBER: 60/120,416  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 60/121,852  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/109,213  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: 60/123,944  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,945  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,948  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,951  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,946  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,949  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/152,524  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: 60/151,114  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: 60/108,029  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: 60/136,436  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,439  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,567  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/137,127  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/137,131  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/141,448  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 60/136,437  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/156,555  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,634  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,653  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/157,280  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,294  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,281  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,282  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/156,633  
PRIOR FILING DATE: 1999-09-29  
NUMBER OF SEQ ID NOS: 146  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 14  
LENGTH: 390  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-876-252-14

Query Match 64.3%; Score 1308.5; DB 10; Length 390;  
Best Local Similarity 65.1%; Pred. No. 4.3e-106;  
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

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QY 5 NSTIALT-SIKISLTFELMSLAIAMGNVVLAFIVDRNLRRSNYPFLNLAIDFV 63
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Db 5 NSTINSLSTRVTLAFPMMSLVAFAIMGNALVILAFVVDKNLRRSYFFLNLAISDFV 64
QY 64 GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYWYRA 123
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 64 GAIAIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYSYRT 124
QY 124 QHSGTWKIATQWAVVIFSFMTNGPMILISDSQWNTTECEBPGLKKWYFALPTSLEFL 183
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 124 QHTGVAKITVLWAVVAVLAVNGPMILVSESKWDSCEBPGFSEBWYLAITSFLEFV 184
QY 184 IPILLVAYSAAHYMSLMKREKLSRCLSHPVLPSSDSSSDHGSQDPPSRATLPARKE 243
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Db 184 IPVILVAYFNMNTYMSLMKRDHLSCQSHRGLTA-VSSNCGHSFGRSLSRSLASTE 243
QY 244 TTASLGSDBSRKSSLLPSIRAYKSNVJASXKGFSLHSDSLAQOREHIELFRARKLAK 303
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 244 VPASFSEQRQRKSSLMFSRRTKNSNTIASXKGSFSQSDVALHQREHIELRARLAK 303
QY 304 STAILLAAPALICAPYSLTVTIYSPFERNLTKSTYHTAFWLQWNSFVNPLYPYLCHK 363
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 304 STAILLGVAVCAVAPSLFTIYLSFYSSATGPKSVWYRIAFWLQWNSFVNPLYPYLCHK 363
QY 364 RFOKAFKILPVRRQSTP--PHNRSIST 369
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 364 RFOKAFKILFCIKQPLPSQHSRVS 390
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## RESULT 8

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US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejltz, Torsten
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: NO. US20030032784A1el G Protein-Coupled Receptors
; FILE REFERENCE: 00231regUS
; CURRENT APPLICATION NUMBER: US/09/852,165
; PRIOR FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-165-2
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Query Match 64.3%; Score 1308.5; DB 10; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;
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QY 5 NSTIALT-SIKISLTFELMSLAIAMGNVVLAFIVDRNLRRSNYPFLNLAIDFV 63
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Db 5 NSTINSLSTRVTLAFPMMSLVAFAIMGNALVILAFVVDKNLRRSYFFLNLAISDFV 64
QY 64 GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYWYRA 123
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 64 GAIAIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYSYRT 124
QY 124 QHSGTWKIATQWAVVIFSFMTNGPMILISDSQWNTTECEBPGLKKWYFALPTSLEFL 183
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 124 QHTGVAKITVLWAVVAVLAVNGPMILVSESKWDSCEBPGFSEBWYLAITSFLEFV 184
QY 184 IPILLVAYSAAHYMSLMKREKLSRCLSHPVLPSSDSSSDHGSQDPPSRATLPARKE 243
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Db 184 IPVILVAYFNMNTYMSLMKRDHLSCQSHRGLTA-VSSNCGHSFGRSLSRSLASTE 243
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QY 244 TTASLGSDBSRKSSLLPSIRAYKSNVJASXKGFSLHSDSLAQOREHIELFRARKLAK 303
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Db 304 STAILLGVAVCAVAPSLFTIYLSFYSSATGPKSVWYRIAFWLQWNSFVNPLYPYLCHK 363
QY 364 RFOKAFKILPVRRQSTP--PHNRSIST 369
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Db 364 RFOKAFKILFCIKQPLPSQHSRVS 390
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## RESULT 9

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US-09-891-138A-6
; Sequence 6, Application US/09891138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: NO. US20030083245A1el Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6
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Query Match 64.3%; Score 1308.5; DB 10; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;
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QY 5 NSTIALT-SIKISLTFELMSLAIAMGNVVLAFIVDRNLRRSNYPFLNLAIDFV 63
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Db 5 NSTINSLSTRVTLAFPMMSLVAFAIMGNALVILAFVVDKNLRRSYFFLNLAISDFV 64
QY 64 GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYWYRA 123
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 64 GAIAIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVSNAYSYRT 124
QY 124 QHSGTWKIATQWAVVIFSFMTNGPMILISDSQWNTTECEBPGLKKWYFALPTSLEFL 183
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Db 124 QHTGVAKITVLWAVVAVLAVNGPMILVSESKWDSCEBPGFSEBWYLAITSFLEFV 184
QY 184 IPILLVAYSAAHYMSLMKREKLSRCLSHPVLPSSDSSSDHGSQDPPSRATLPARKE 243
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 184 IPVILVAYFNMNTYMSLMKRDHLSCQSHRGLTA-VSSNCGHSFGRSLSRSLASTE 243
QY 244 TTASLGSDBSRKSSLLPSIRAYKSNVJASXKGFSLHSDSLAQOREHIELFRARKLAK 303
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 244 VPASFSEQRQRKSSLMFSRRTKNSNTIASXKGSFSQSDVALHQREHIELRARLAK 303
QY 304 STAILLAAPALICAPYSLTVTIYSPFERNLTKSTYHTAFWLQWNSFVNPLYPYLCHK 363
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 304 STAILLGVAVCAVAPSLFTIYLSFYSSATGPKSVWYRIAFWLQWNSFVNPLYPYLCHK 363
QY 364 RFOKAFKILPVRRQSTP--PHNRSIST 369
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 364 RFOKAFKILFCIKQPLPSQHSRVS 390
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## RESULT 10

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US-10-052-193-2
; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-052-193-2

Query Match      64.3%; Score 1308.5; DB 13; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFELMSLAIATMGNVVTIAFIYDRNIRHRSNYFFLNLAIADFFV 63
DB 5 NSTIMLSISTRVTTLAFPMSLVAFALMGNALVILAFVVDKNIRHRSYFFFLNLAIADFFV 64
QY 64 GAIAIPLYPSSLTFTWTSKQACVFWLITDYLLCTASVYNYILSYDRYQSVSNVWYRA 123
DB 65 GVISLPLYPHLPFLFMDGKCEICVFWLITDYLLCTASVYNYILSYDRYQSVSNVWYRT 124
QY 124 QHSGTWKTIATQWVAWVIFSFMTNGPMILISDSWQNSTECCBPGFKKWFALPTSLLEFL 183
DB 125 QHTGVLKIVTLVAVVAVLAFVNGPMILVSESKWDEGCEBGFSEWYILAITSFLEFV 184
QY 184 IPIILVAFSAHIYWSLWKREKLSRCLSHPVLPSSDSSDHGSCRODDSPATTPARKE 243
DB 185 IPIILVAFSAHIYWSLWKREKLSRCLSHPVLPSSDSSDHGSCRODDSPATTPARKE 243
QY 244 TTASIGSDKSRKSSLLPSIRAYKSNVYASIMGFLSHSDSLALQOREHIELFRARKLAK 303
DB 244 VPASFHSERQRRKSSLMFSRRTKMSNTIASMGFSQSDSVLHOREHVELLRARRLAK 303
QY 304 SLAIIILAFALCWAAPYSLTFTVYISFPPERNLTKSTWYHTAFWLQWPNFVNPLYPPLCHK 363
DB 304 SLAIIILGFVAVCMAPYSLTFTVILSFYSSATGPKSVYRIAFWLQWPNFVNPLYPPLCHK 363
QY 364 RFQKAFKLILPVROSTP-PHNRSTST 389
DB 364 RFQKAFKLIFCIKKOPLPFSQHSRSVSS 390

RESULT 11
US-10-225-567A-629
; Sequence 629, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 629
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-225-567A-629

Query Match      64.3%; Score 1308.5; DB 14; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.3e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFELMSLAIATMGNVVTIAFIYDRNIRHRSNYFFLNLAIADFFV 63
DB 5 NSTIMLSISTRVTTLAFPMSLVAFALMGNALVILAFVVDKNIRHRSYFFFLNLAIADFFV 64
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DB 125 QHTGVLKIVTLVAVVAVLAFVNGPMILVSESKWDEGCEBGFSEWYILAITSFLEFV 184
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QY 244 TTASIGSDKSRKSSLLPSIRAYKSNVYASIMGFLSHSDSLALQOREHIELFRARKLAK 303
DB 244 VPASFHSERQRRKSSLMFSRRTKMSNTIASMGFSQSDSVLHOREHVELLRARRLAK 303
QY 304 SLAIIILAFALCWAAPYSLTFTVYISFPPERNLTKSTWYHTAFWLQWPNFVNPLYPPLCHK 363
DB 304 SLAIIILGFVAVCMAPYSLTFTVILSFYSSATGPKSVYRIAFWLQWPNFVNPLYPPLCHK 363
QY 364 RFQKAFKLILPVROSTP-PHNRSTST 389
DB 364 RFQKAFKLIFCIKKOPLPFSQHSRSVSS 390

RESULT 12
US-10-272-983-14
; Sequence 14, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390

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TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-272-983-14

Query Match 64.3%; Score 1308.5; DB 14; Length 390;  
Best Local Similarity 65.1%; Pred. No. 4.3e-106;  
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY NSTIATL-SIKISLFLMSLAIAMGNVVLAFIVDRNLHRSNYPFLNLAIDPFV 63  
DB NSTINLSLSTRVLAFFMSLVAFAMLGALVLAFLVDRNLHRSSYFFLNLAIIDPFV 64  
QY GAIAPLYIPSSLTWTSGKACVFWLITDYLCTASVNNIVLISYDRYQSVSNAYWYRA 123  
DB GAVISILYIPHTLFEBDFGKEICVFWLITDYLCTASVNNIVLISYDRYQSVSNAYWYRA 124  
QY QHSGTWKIAITONAVVIFSPMTNGPMILISDSQNSTTECEPGLKKYFALFTSLLEFL 183  
DB QHTGVAKIYITLWAVVAVLAFVNGPMILVSESWKDSCEPGLFSEWYLAITSFLEFV 184  
QY IPIILVAFSAHYWLSLMREKLSRCLSHPVLPSSSDSHGSCQDPDSRATLPARKE 243  
DB IPIILVAFSAHYWLSLMREKLSRCLSHPVLPSSSDSHGSCQDPDSRATLPARKE 243  
QY TTSLSGDSRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLALQOREHIEFPARKLAK 303  
DB VPASFSEQRKSSLMPSRRTMGNTIASKMGFSQSDSVALLHGREHIELARARLAK 303  
QY SLAILLAFAICAPYSLTIVYISFPERNLTKSTYHTAFWLOMNSFVNPLYPPLCHK 363  
DB SLAILGVFAVCAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOMNSFVNPLYPPLCHK 363  
QY RPOKAFKLIPVROSTP--PHNSIST 389  
DB RPOKAFKLIPVROSTP--PHNSIST 389  
QY RPOKAFKLIPVROSTP--PHNSIST 390  
DB RPOKAFKLIPVROSTP--PHNSIST 390

## RESULT 13

US-10-354-769-2  
Sequence 2, Application US/10354769  
Publication No. US20030149242A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer Inc.  
APPLICANT: O'Reilly, Mark A.  
APPLICANT: Peter, Beate  
TITLE OF INVENTION: NOVEL POLYPEPTIDE  
FILE REFERENCE: PCT0373B  
CURRENT APPLICATION NUMBER: US/10/354,769  
CURRENT FILING DATE: 2003-01-30  
PRIOR APPLICATION NUMBER: US 09/698,801  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 60/211,243  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: GB 9925641.4  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: GB 0009973.9  
PRIOR FILING DATE: 2000-04-20  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent version 3.1  
SEQ ID NO 2  
LENGTH: 390  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-354-769-2

Query Match 64.3%; Score 1308.5; DB 14; Length 390;  
Best Local Similarity 65.1%; Pred. No. 4.3e-106;  
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY NSTIATL-SIKISLFLMSLAIAMGNVVLAFIVDRNLHRSNYPFLNLAIDPFV 63  
DB NSTINLSLSTRVLAFFMSLVAFAMLGALVLAFLVDRNLHRSSYFFLNLAIIDPFV 64

QY GAIAPLYIPSSLTWTSGKACVFWLITDYLCTASVNNIVLISYDRYQSVSNAYWYRA 123  
DB GAVISILYIPHTLFEBDFGKEICVFWLITDYLCTASVNNIVLISYDRYQSVSNAYWYRA 124  
QY QHSGTWKIAITONAVVIFSPMTNGPMILISDSQNSTTECEPGLKKYFALFTSLLEFL 183  
DB QHTGVAKIYITLWAVVAVLAFVNGPMILVSESWKDSCEPGLFSEWYLAITSFLEFV 184

QY IPIILVAFSAHYWLSLMREKLSRCLSHPVLPSSSDSHGSCQDPDSRATLPARKE 243  
DB IPIILVAFSAHYWLSLMREKLSRCLSHPVLPSSSDSHGSCQDPDSRATLPARKE 243  
QY TTSLSGDSRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLALQOREHIEFPARKLAK 303  
DB VPASFSEQRKSSLMPSRRTMGNTIASKMGFSQSDSVALLHGREHIELARARLAK 303  
QY SLAILLAFAICAPYSLTIVYISFPERNLTKSTYHTAFWLOMNSFVNPLYPPLCHK 363  
DB SLAILGVFAVCAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOMNSFVNPLYPPLCHK 363  
QY RPOKAFKLIPVROSTP--PHNSIST 389  
DB RPOKAFKLIPVROSTP--PHNSIST 389  
QY RPOKAFKLIPVROSTP--PHNSIST 390  
DB RPOKAFKLIPVROSTP--PHNSIST 390

## RESULT 14

US-10-393-807-14  
Sequence 14, Application US/10393807  
Publication No. US20030175891A1  
GENERAL INFORMATION:  
APPLICANT: Bang, Huong T.  
APPLICANT: Liaw, Chen W.  
APPLICANT: Lin, I-tin  
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
FILE REFERENCE: AREN0050  
CURRENT APPLICATION NUMBER: US/10/393,807  
CURRENT FILING DATE: 2003-03-21  
PRIOR APPLICATION NUMBER: US/09/417,044  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: 60/109,213  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: 60/120,416  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 60/121,851  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/123,946  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,949  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/136,436  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,437  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,439  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,567  
PRIOR FILING DATE: 1999-05-28  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 14  
LENGTH: 390  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-393-807-14

Query Match 64.3%; Score 1308.5; DB 14; Length 390;  
Best Local Similarity 65.1%; Pred. No. 4.3e-106;  
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY NSTIATL-SIKISLFLMSLAIAMGNVVLAFIVDRNLHRSNYPFLNLAIDPFV 63  
DB NSTINLSLSTRVLAFFMSLVAFAMLGALVLAFLVDRNLHRSSYFFLNLAIIDPFV 64

Db 5 NSTILSLSTRVTLAFENSLVAFALMGNALVILAEVVDKRLRHRSYFFLNLAISDFEV 64  
Qy 64 GAIAIPLYIPSSLYWTSGKQACVFWLITDYLLCTASVYNYVILISYDRQSVSNVWYRA 123  
Db 65 GVISIPLYIPHLFEMDEGKEICVFWLITDYLLCTASVYNYVILISYDRQSVSNVWYRA 124  
Qy 124 OHSGTWKATQWVAWVAFSFMNGPMILISDSWQNSTECPGFLKMYFALPTSLEFL 183  
Db 125 QHTGVLTITVTLVAVWVLAFLVNGPMIIVSESKDEGSECEGPFSEWYILATISFLEFV 184  
Qy 184 IPILVAFSAHIYWSLWKREKLSRCLSHPVLPSSSSSDHSGSCRODDSPATLPARKE 243  
Db 185 IPVILVAFNMNIYWSLWKRDHLSCQSHPGTLA-VSSNICGHSFRGRLSRSLSASTE 243  
Qy 244 TTASIGSDKSRKSSLLPSIRAYKSNVYASKMGFLSHSDSLALQOREHIELEFPAKRLAK 303  
Db 244 VPASHSERQRKSSLMFSSRTKXNSNTIASKMGSSQSDSVALLQREHVELLRARRLAK 303  
Qy 304 SIAIILAFATCMAPYSLTVTYISFEPERNLTGSTWYHTAFWLQWPNFVNPFYPLCHK 363  
Db 304 SIAIILGVFAVCMAPYSLTFTIVLSFYSSATGPKSVWYRIAFWLQWPNFVNPFYPLCHK 363  
Qy 364 RFQKAFKLIFCTIKQPLPSQHSRSVSS 390  
Db 364 RFQKAFKLIFCTIKQPLPSQHSRSVSS 390

## RESULT 15

US-10-417-820A-14

Sequence 14, Application US/10417820A

Publication No. US20030229216A1

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Liaw, Chen W.

APPLICANT: Lowitz, Kevin

APPLICANT: Chalmers, Derek T.

APPLICANT: Behan, Dominic P.

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

FILE REFERENCE: 7.US28.CON

CURRENT APPLICATION NUMBER: US/10/417,820A

CURRENT FILING DATE: 2003-04-16

PRIOR APPLICATION NUMBER: 09/416,760

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: 60/110,060

PRIOR FILING DATE: 1998-11-27

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,852

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/109,213

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: 60/123,944

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,945

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,948

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,951

PRIOR FILING DATE: 1999-03-12

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 155

SOFTWARE: PatentIn version 3.2

SEQ ID NO 14

LENGTH: 390

TYPE: PRT

ORGANISM: Homo sapiens

US-10-417-820A-14

Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;  
Qy 5 NSTIALT-SIKISLTFMNLALAIIMGNVVIILAFIVDRNLRHRSNYFFLNLAISDFEV 63  
Db 5 NSTILSLSTRVTLAFENSLVAFALMGNALVILAEVVDKRLRHRSYFFLNLAISDFEV 64  
Qy 64 GAIAIPLYIPSSLYWTSGKQACVFWLITDYLLCTASVYNYVILISYDRQSVSNVWYRA 123  
Db 65 GVISIPLYIPHLFEMDEGKEICVFWLITDYLLCTASVYNYVILISYDRQSVSNVWYRA 124  
Qy 124 OHSGTWKATQWVAWVAFSFMNGPMILISDSWQNSTECPGFLKMYFALPTSLEFL 183  
Db 125 QHTGVLTITVTLVAVWVLAFLVNGPMIIVSESKDEGSECEGPFSEWYILATISFLEFV 184  
Qy 184 IPILVAFSAHIYWSLWKREKLSRCLSHPVLPSSSSSDHSGSCRODDSPATLPARKE 243  
Db 185 IPVILVAFNMNIYWSLWKRDHLSCQSHPGTLA-VSSNICGHSFRGRLSRSLSASTE 243  
Qy 244 TTASIGSDKSRKSSLLPSIRAYKSNVYASKMGFLSHSDSLALQOREHIELEFPAKRLAK 303  
Db 244 VPASHSERQRKSSLMFSSRTKXNSNTIASKMGSSQSDSVALLQREHVELLRARRLAK 303  
Qy 304 SIAIILAFATCMAPYSLTVTYISFEPERNLTGSTWYHTAFWLQWPNFVNPFYPLCHK 363  
Db 304 SIAIILGVFAVCMAPYSLTFTIVLSFYSSATGPKSVWYRIAFWLQWPNFVNPFYPLCHK 363  
Qy 364 RFQKAFKLIFCTIKQPLPSQHSRSVSS 390  
Db 364 RFQKAFKLIFCTIKQPLPSQHSRSVSS 390

Search completed: August 3, 2005, 02:00:31

Job time : 160 secs

Query Match 64.3%; Score 1308.5; DB 15; Length 390;  
Best Local Similarity 65.1%; Pred. No. 4.3e-106;

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 3, 2005, 01:42:02 ; Search time 165 Seconds  
(without alignments)  
911.817 Million cell updates/sec

Title: US-10-626-398-10

Perfect score: 2036  
Sequence: 1 MLANNSTALTSIKISLTLF.....LKILPVROSTPPHNSISR 389

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1980s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2025	99.5	389	5	AAM50567 Guinea p.i
2	1308.5	64.3	390	3	AA02831 Human G p
3	1308.5	64.3	390	3	AA071297 Human G p
4	1308.5	64.3	390	4	AA062445 Human GPC
5	1308.5	64.3	390	4	AA064477 Human G p
6	1308.5	64.3	390	4	AA073622 Human G p
7	1308.5	64.3	390	5	AAM53050 Human G p
8	1308.5	64.3	390	5	ABP98629 Human his
9	1308.5	64.3	390	5	AB078276 Amino aci
10	1308.5	64.3	390	5	AAM50564 Human his
11	1308.5	64.3	390	5	AA066023 Human his
12	1308.5	64.3	390	5	AAU74906 Amino aci
13	1308.5	64.3	390	6	ABG71960 Human G-p
14	1308.5	64.3	390	6	ABU92265 Human G p
15	1308.5	64.3	390	6	ABP81727 Human his
16	1308.5	64.3	390	6	AA036417 Human H4
17	1308.5	64.3	390	7	ADG98760 Human GPC
18	1308.5	64.3	390	7	ADJ26923 Human end
19	1308.5	64.3	390	8	ADG86375 Human end
20	1308.5	64.3	390	8	ADJ88376 Novel hum
21	1308.5	64.3	390	8	AD005720 Human his
22	1308.5	64.3	390	8	AD029496 Human GPC
23	1308.5	64.3	390	8	ADP20168 Human G p
24	1308.5	64.3	390	8	ADQ75074 Human G p
25	1308.5	64.3	391	5	AAM53052 Human G p

26	1308.5	64.3	392	5	AAM53053 Human G p
27	1306.5	64.2	390	4	AAM51410 Human GPR
28	1306.5	64.2	390	6	AA036416 Human H4
29	1303.5	64.0	390	8	ADG86522 Human end
30	1244	61.1	391	5	AAM50565 Mouse his
31	1244	61.1	391	8	AD029497 Mouse GPC
32	1235.5	60.7	391	5	AAM50566 Rat hist
33	1166	57.3	357	6	AA036415 Human H4
34	1048.5	51.5	336	6	AA036414 Human H4
35	694.5	34.1	413	2	AA022207 G-protein
36	694.5	34.1	413	3	AA015383 Rat G-pro
37	689.5	33.9	445	2	AA029275 Human MAC
38	689.5	33.9	445	2	AA063222 Human G p
39	689.5	33.9	445	2	AA067830 Human mus
40	689.5	33.9	445	3	AA092218 Human his
41	689.5	33.9	445	4	AA030627 A human h
42	689.5	33.9	445	5	AB079792 Human his
43	689.5	33.9	445	6	AB043667 Human his
44	689.5	33.9	445	6	ABP57425 Human his
45	689.5	33.9	445	6	AA019746 Human his

## ALIGNMENTS

RESULT 1	
AAM50567	
ID AAM50567 standard; protein; 389 AA.	
XX	
AC AAM50567;	
XX	
DT 18-MAR-2002 (first entry)	
XX	
DE Guinea pig histamine H4 receptor.	
XX	
KM Histamine H4 receptor; guinea pig; antispasmodic; antiallergenic;	
KM antiinflammatory; cardiac; circulatory; antidiabetic; laxative;	
KM diagnosis; gene therapy.	
XX	
OS Cavia porcellus.	
XX	
PN WO200192485-A1.	
XX	
PD 06-DEC-2001.	
XX	
PF 22-FEB-2001; 2001MO-US005914.	
XX	
PR 31-MAY-2000; 2000US-0208260P.	
XX	
PA (ORTH ) ORTHO-MCNEIL PHARM INC.	
XX	
PI Lovenberg T, Liu C;	
XX	
PT WPI; 2002-114339/15.	
DR N-PSDB; AAT0983.	
XX	
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding	
PT the protein; useful in gene therapy for treating diseases where it is	
PT beneficial to elevate mammalian histamine H4 receptor activity.	
XX	
PS Claim 13; Fig 6C; 92pp; English.	
XX	
CC The present sequence is that of a guinea pig histamine receptor of the H4	
CC subtype, as predicted from a cDNA clone isolated from a bone marrow	
CC library. The invention provides mammalian (human, mouse, rat and guinea	
CC pig) histamine H4 receptor nucleic acid molecules (see AAT0980-83) and	
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in	
CC recombinant host cells that produce active recombinant protein. The	
CC pharmacology of known histamine ligands is demonstrated. Mammalian	
CC histamine H4 receptor may be used in gene therapy for the treatment of	
CC diseases where it is beneficial to elevate mammalian histamine H4	
CC receptor activity. Recombinant protein is useful for identifying	
CC modulators of the histamine H4 receptor. Such modulators may be useful	

CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
 CC diabetes mellitus, hypoglycemia, constipation, arrhythmia, disorders of  
 CC the neuroendocrine system, stress and spasticity

XX Sequence 389 AA;

Query Match 99.5%; Score 2025; DB 5; Length 389;  
 Best Local Similarity 99.7%; Pred. No. 8e-204;  
 Matches 388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MANNSTLTSIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRNSNYFFLMAIAD 60
DB 1 MANNSTLTSIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRNSNYFFLMAIAD 60
QY 61 FVGAIAIPLYPSSLTWTSGKQACVFWLITDYLTCTASVYNIVLISYDRQSVSNMAY 120
DB 61 FVGAIAIPLYPSSLTWTSGKQACVFWLITDYLTCTASVYNIVLISYDRQSVSNMAY 120
QY 121 YPAQSGTWKIAITQWVAWVIFSFMTNGPMILISDSQNSSTCEPGLKKWYFALPTSL 180
DB 121 YPAQSGTWKIAITQWVAWVIFSFMTNGPMILISDSQNSSTCEPGLKKWYFALPTSL 180
QY 181 EFLIPLILVAYSAHIYWSLWKREKLSRCLSHPVLPDSSSDHGHSCRODPDSRATTPA 240
DB 181 EFLIPLILVAYSAHIYWSLWKREKLSRCLSHPVLPDSSSDHGHSCRODPDSRATTPA 240
QY 241 RKETIASGDSKSRKSSLLPSTIRAYKNSNVIAASKGFLSHSDSLAQOREHIELEFRARK 300
DB 241 RKETIASGDSKSRKSSLLPSTIRAYKNSNVIAASKGFLSHSDSLAQOREHIELEFRARK 300
QY 301 LAKSLAIIILAAFAICWAPYSLTTVIYSPFERNLTKSTWYHTAFWLQWNSFVNPLVPL 360
DB 301 LAKSLAIIILAAFAICWAPYSLTTVIYSPFERNLTKSTWYHTAFWLQWNSFVNPLVPL 360
QY 361 CHKRFQAKFLKILPVRRQSTPPHNSIST 389
DB 361 CHKRFQAKFLKILPVRRQSTPPHNSIST 389

```

RESULT 2

AAB02831 ID AAB02831 standard; protein; 390 AA.

XX AAB02831;

DT 22-AUG-2000 (first entry)

XX Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.

XX Human; G protein coupled receptor; GPCR; transmembrane receptor;  
 XX identification; agonist; screening; therapeutic; pharmaceutical; mutant.

OS Homo sapiens.

PN WO200022131-A2.

PD 20-APR-2000.

PF 13-OCT-1999; 99WO-US024065.

PR 13-OCT-1999; 98US-00170496.

PR 12-NOV-1998; 98US-0108029P.

PR 20-NOV-1998; 98US-0109213P.

PR 27-NOV-1998; 98US-0110060P.

PR 16-FEB-1999; 99US-0120416P.

PR 26-FEB-1999; 99US-0121852P.

PR 12-MAR-1999; 99US-0123944P.

PR 12-MAR-1999; 99US-0123945P.

PR 12-MAR-1999; 99US-0123946P.

PR 12-MAR-1999; 99US-0123948P.

PR 12-MAR-1999; 99US-0123949P.

PR 12-MAR-1999; 99US-0123951P.

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PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 28-MAY-1999; 99US-0137567P.
PR 29-JUN-1999; 99US-0141448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0155224P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.

```

XX (AREN-) ARENA PHARM INC.

XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT,

PI Gore M, Hlaw CW, Lin I, Lowitz K, White C;

XX WPI; 2000-317986/27.

DR N-PSDB; AAA46023.

PT Non-endogenous, human G protein-coupled receptors for screening receptor,  
 XX Inverse or partial agonists useful as therapeutic agents.

XX Example 1; Page 89-90; 187pp; English.

CC The present invention describes transmembrane receptors, preferably human  
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is  
 CC unknown (orphan GPCR receptors). More specifically the present invention  
 CC relates to non-endogenous, constitutively activated versions of a human  
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
 CC identification of candidate compounds as receptors agonists, inverse  
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017  
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
 CC exemplification of the present invention

XX Sequence 390 AA;

Query Match 64.3%; Score 1308.5; DB 3; Length 390;

Best Local Similarity 65.1%; Pred. No. 1.9e-128; Mismatches 84; Indels 3; Gaps 3;

XX Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

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QY 5 NSTIALT-SIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRNSNYFFLMAIADFV 63
DB 5 NSTIALT-SIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRNSNYFFLMAIADFV 63
QY 64 GAIAPLYIPSSLTWTSGKQACVFWLITDYLTCTASVYNIVLISYDRQSVSNMAYRA 123
DB 64 GAIAPLYIPSSLTWTSGKQACVFWLITDYLTCTASVYNIVLISYDRQSVSNMAYRA 123
QY 125 QHTGVAKIVTLVAVVAVVAFVNGPMILVSEWKBGSCBCEGFSEWITLITSFLETV 184
DB 125 QHTGVAKIVTLVAVVAVVAFVNGPMILVSEWKBGSCBCEGFSEWITLITSFLETV 184
QY 184 IPIILVAYSAHIYWSLWKREKLSRCLSHPVLPDSSSDHGHSCRODPDSRATTPARKE 243
DB 184 IPIILVAYSAHIYWSLWKREKLSRCLSHPVLPDSSSDHGHSCRODPDSRATTPARKE 243
QY 244 TPASFSERQRKSSLSMSSRTKNSNTIASMGFSQSDVALHQREHIELEFRARLAK 303
DB 244 TPASFSERQRKSSLSMSSRTKNSNTIASMGFSQSDVALHQREHIELEFRARLAK 303
QY 304 SIATILAAFAICWAPYSLTTVIYSPFERNLTKSTWYHTAFWLQWNSFVNPLVPLCHK 363
DB 304 SIATILAAFAICWAPYSLTTVIYSPFERNLTKSTWYHTAFWLQWNSFVNPLVPLCHK 363

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OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Domain 19..41  
 FT Domain /label= Transmembrane\_domain\_1  
 FT Domain 52..74  
 FT Domain /label= Transmembrane\_domain\_2  
 FT Domain 86..110  
 FT Domain /label= Transmembrane\_domain\_3  
 FT Domain 128..146  
 FT Domain /label= Transmembrane\_domain\_4  
 FT Domain 172..194  
 FT Domain /label= Transmembrane\_domain\_5  
 FT Domain 305..326  
 FT Domain /label= Transmembrane\_domain\_6  
 FT Domain 342..360  
 FT Domain /label= Transmembrane\_domain\_7  
 XX WO200185793-A2.  
 PD 15-NOV-2001.  
 PF 08-MAY-2001; 2001WO-US014750.  
 PR 08-MAY-2000; 2000US-0203108P.  
 XX (PHAA ) PHARMACIA & UPJOHN CO.  
 PA Lind P, Sejlitz T, Vogel G, Wood LS;  
 PI WPI; 2002-062240/08.  
 DR N-PSDB; ABA02496.  
 XX New polynucleotide, useful for identifying modulator compounds which are  
 PT used for treating psoriasis, schizophrenia, diabetes, encodes the novel G  
 PT protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).  
 PS Claim 31; Page 63; 100pp; English.  
 CC This sequence represents a novel human G protein-coupled receptor (GPCR)  
 CC designated nGPCR-2067. Like all GPCRs, nGPCR-2067 has 7 putative  
 CC transmembrane domains and is involved in signal transduction. The  
 CC invention also relates to expression vectors and host cells comprising  
 CC nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-  
 CC 2067, to antibodies specific for nGPCR-2067, to drug screening methods  
 CC that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067  
 CC nucleic acid sequences may be used to isolate nGPCR-2067 allelic variants  
 CC and species homologues and may also be used in genetic mapping. The  
 CC invention also discloses the use of nGPCR-2067 nucleic acids in screening  
 CC for a predisposition to nGPCR-2067-associated hereditary mental  
 CC disorders, or for the diagnosis of these disorders. nGPCR-2067 nucleic  
 CC acids may additionally be used to generate transgenic animals, including  
 CC knockout animals, which may provide an insight into treating a variety of  
 CC human disorders, and may also be used in the design of antisense  
 CC molecules for suppressing expression of nGPCR-2067 in cells. nGPCR-2067,  
 CC and nGPCR-2067 modulators may be used to treat a wide variety of medical  
 CC conditions, particularly mental disorders, central nervous system  
 CC diseases, and metabolic diseases. Diseases that may be treated include  
 CC viral infections, particularly HIV-1 or HIV-2 infections; pain; central  
 CC nervous system, neurological and psychotic disorders such as Huntington's  
 CC disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,  
 CC dementia, Alzheimer's disease, and Parkinson's disease; proliferative  
 CC disorders such as cancer, benign prostatic hypertrophy and psoriasis;  
 CC metabolic disorders such as diabetes, dyslipidaemia, obesity, and  
 CC anorexia; thyroid disorders; cardiovascular diseases such as hypotension,  
 CC hypertension, thrombosis, myocardial infarction, cardiomyopathies, and  
 CC atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,  
 CC rheumatoid arthritis); hormonal disorders; and renal failure

Sequence 390 AA;

Query Match 64.3%; Score 1308.5; DB 5; Length 390;  
 Best Local Similarity 65.1%; Pred. No. 1.9e-128;

Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;  
 QY 5 NSTIALT-SIKISLFLMSLAIAIMLGNVVILAFIDRNLRHSNFFNLAIADFPV 63  
 DB 5 NSTINLSLSTRTVTLAFPMSLVAFALMGNALVILAFVDDKLRHSSYFFNLAIADFPV 64  
 QY 64 GAIALPLYIPSSLTLYWTSKQACVFWLITDYLCTASYNYNVLISYDRQSVSNWYRA 123  
 DB 65 GVISIPLYIPHTLPFMDFGKEICVFWLITDYLCTASYNYNVLISYDRLSVSNVSYRT 124  
 QY 124 QHSGTWKATQVMVWVWISFMTNGPMILISDSWQNSTECCEGFLKRYFALPTSLLEFL 163  
 DB 125 QHTGVLKVTTLVAVWVILAVNGPMILVSEWKGSECEGFPSEWTLAITSFLEPV 184  
 QY 184 IPILVAFSAHYVSLWKRKLSRCLSPVLPDSSSDSHGSRQPDSPATYPARKE 243  
 DB 185 IPVILVAFENMNIYVSLMKRDLHSRCQHPGLTA-VSSNICGHSRGRSLSSRSLSAGE 243  
 QY 244 TTSLSGDSKSRKSSLLPSIRAYKSNVYASKGFLSHSDSLAQOREHIEFLFRARKLAK 303  
 DB 244 VPASFHSERQRKSSLSMFSSRTKNNSNTIASKGSFQSDSVLAHQREHVELLRARLAK 303  
 QY 304 SLATLLAFATCMAPYSLTITYISFFPERNLTKSTWYTAFTWLFQFNSTFVPLPLCHK 363  
 DB 304 SLATLLGVFAVCWAPYSLFTVLSFYSATGPKSVYRIAFWLFQFNSTFVPLPLCHK 363  
 QY 364 RFOKAFLLKILPVRSOSTP-PHNRISIST 389  
 DB 364 RFOKAFLLKIFCTIKQPLPSQHSRSVSS 390  
 RESULT 8  
 ABP98629  
 ID ABP98629 standard; protein; 390 AA.  
 XX ABP98629;  
 AC 13-JUN-2003 (first entry)  
 DT 13-JUN-2003 (first entry)  
 DE Human histamine receptor SP9144.  
 XX human; histamine receptor; chromosome 18; anti-inflammatory;  
 KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;  
 KW anti-migraine; cardiac; anti-rheumatic; anti-arthritis; antipsoriatic;  
 KW neuroprotective; inflammatory; asthma; allergy; atopic dermatitis;  
 KW myocardial infarction; migraine; chronic obstructive pulmonary disease;  
 KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;  
 KW psoriasis; receptor.  
 XX OS Homo sapiens.  
 XX US6204017-B1.  
 PN 20-MAR-2001.  
 XX 07-OCT-1999; 99US-00414010.  
 PF 07-OCT-1999; 99US-00414010.  
 PR 07-OCT-1999; 99US-00414010.  
 XX (SCHE ) SCHERING CORP.  
 PA Behan JX, Hedrick JA, Laz TM, Monema FJ, Morse KL, Umland SP,  
 PI Wang S;  
 PI WPI; 2002-442063/47.  
 DR N-PSDB; AB280663.  
 XX New nucleic acid encoding antigenic part of human histamine receptor,  
 PT useful for preparing antibodies, e.g. for treating-histamine related  
 PT disorders.  
 XX Example 1; Col 27-30; 19pp; English.

This sequence represents the amino acid sequence of a human histamine receptor (HR) designated SP9144. The sequence was isolated by searching databases with the sequence of known G-coupled protein receptor (GPCR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunofluorescence chromatography. In immunoblotting of histamine receptor, to identify cDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.

Sequence 390 AA:

Query Match 64.3%; Score 1308.5; DB 5; Length 390;  
Best Local Similarity 65.1%; Pred. No. 1.9e-128;  
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

```

QY 5 NSTIATLT-SIKISLTFMLSLTAITMLGNVNVVLAFLVDBNLHRNSYFPLNLAIDFFV 63
DB 5 NSTIINSLSTRVTLAFPMSLVAFALMLGNALVILAFVDDKULHRSSYFPLNLAISDFV 64
QY 64 GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLISYDRYQSVSNVAYRA 123
DB 65 GVISITPLYIPHTLFENDFGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVSNVAYRT 124
QY 124 QHSGTWKIAITQWVAWVIFSPMTNGPMILISDSQNSTTECEPGLKKWYFALPTSLEFL 183
DB 125 QHTGVAKIYITLWVAWVLAFLVNGPMILVSESWKDEGSECEPGEFSEWYLAITSFLEFV 184
QY 184 IPIILVAYSANHYWLSMKREKLSRCLSHPVLPSSDSSSDHSGSCODPDPRATLPARKE 243
DB 185 IPIILVAYFMNHYWLSMKRDLHSLRCQSHPLGLTA-VSSNLCGHSFGRLSSRSLSASTE 243
QY 244 TTSASLSDSKSRKSSLLPSIRAYKSNVNIASKGFLSHSDSLALQOREHIELFRARLAK 303
DB 244 VPASFSFSEORRRSSLSMFSSRTGNSNTTASKKGSQSGSVALLHREHIELRARLAK 303
QY 304 SLAIIILAAFAICWAPYSLTTVIYSPPERNLTKSTWYHTAFWLQWNSFVNPPLYPLCHK 363
DB 304 SLAIIILGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPPLYPLCHK 363
QY 364 RFQKAFKLIPVRROSTP-PHNSISIT 389
DB 364 RFQKAFKLIPCIKQPLPSQHSRVS 390

```

# RESULT 9

ABR78276 standard; protein; 390 AA.

AC ABR78276;

DT 05-DEC-2002 (first entry)

DE Amino acid sequence of human histamine receptor.

XX Human; histamine receptor; receptor; inflammation; asthma; allergy;  
XX atopic dermatitis; stroke; myocardial infarction; migraine;  
XX chronic obstructive pulmonary disease (COPD); rheumatoid arthritis;  
XX multiple sclerosis; inflammatory bowel disease; psoriasis;  
XX intracellular second messenger pathway; cellular growth rate;  
XX hormone secretion.

OS Homo sapiens.

XX US2002098539-A1.

XX 25-JUL-2002.

PF 19-MAR-2001; 2001US-00812216.

XX 07-OCT-1999; 99US-00414010.

XX (BEHN) BEHN J X.  
PA (HEDR) HEDRICK J A.  
PA (LAZT) LAZ T M.  
PA (MONS) MONSMA F J.  
PA (MORS) MORSE K L.  
PA (UMLA) UMLAND S P.  
PA (WANG) WANG S.

XX Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP,  
PI Wang S;  
PI  
XX WPI: 2002-673827/72.  
DR N-PSDB; ABR78739.

PT Novel mammalian histamine receptor polypeptide useful for identifying  
agonist or antagonist for treating diseases such as inflammation, asthma,  
stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.

XX Claim 2; Page 16-17; 21pp; English.

XX The present sequence represents a histamine receptor. The polypeptide is  
CC useful for identifying an agonist or antagonist of a mammalian histamine  
CC receptor. It is useful as an antigen to elicit the production of  
CC antibodies. The histamine receptor polypeptide and polynucleotide are  
CC useful in the treatment and management of diseases such as inflammation,  
CC asthma, allergy, atopic dermatitis, stroke, myocardial infarction,  
CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid  
CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.  
CC They are also useful for modulating intracellular second messenger  
CC pathway activated through histamine receptors (cyclic-AMP, calcium,  
CC inositol phosphate and mitogen activated protein (MAP) kinase), changes  
CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca<sup>2+</sup>  
CC mobilization, mitogenic effects, etc

XX Sequence 390 AA:

Query Match 64.3%; Score 1308.5; DB 5; Length 390;  
Best Local Similarity 65.1%; Pred. No. 1.9e-128;  
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

```

QY 5 NSTIATLT-SIKISLTFMLSLTAITMLGNVNVVLAFLVDBNLHRNSYFPLNLAIDFFV 63
DB 5 NSTIINSLSTRVTLAFPMSLVAFALMLGNALVILAFVDDKULHRSSYFPLNLAISDFV 64
QY 64 GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLISYDRYQSVSNVAYRA 123
DB 65 GVISITPLYIPHTLFENDFGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVSNVAYRT 124
QY 124 QHSGTWKIAITQWVAWVIFSPMTNGPMILISDSQNSTTECEPGLKKWYFALPTSLEFL 183
DB 125 QHTGVAKIYITLWVAWVLAFLVNGPMILVSESWKDEGSECEPGEFSEWYLAITSFLEFV 184
QY 184 IPIILVAYSANHYWLSMKREKLSRCLSHPVLPSSDSSSDHSGSCODPDPRATLPARKE 243
DB 185 IPIILVAYFMNHYWLSMKRDLHSLRCQSHPLGLTA-VSSNLCGHSFGRLSSRSLSASTE 243
QY 244 TTSASLSDSKSRKSSLLPSIRAYKSNVNIASKGFLSHSDSLALQOREHIELFRARLAK 303
DB 244 VPASFSFSEORRRSSLSMFSSRTGNSNTTASKKGSQSGSVALLHREHIELRARLAK 303
QY 304 SLAIIILAAFAICWAPYSLTTVIYSPPERNLTKSTWYHTAFWLQWNSFVNPPLYPLCHK 363
DB 304 SLAIIILGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPPLYPLCHK 363
QY 364 RFQKAFKLIPVRROSTP-PHNSISIT 389
DB 364 RFQKAFKLIPCIKQPLPSQHSRVS 390

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# RESULT 10

AAM50564  
 ID AAM50564 standard; protein; 390 AA.  
 AC AAM50564;  
 XX  
 DT 18-MAR-2002 (first entry)  
 DE Human histamine H4 receptor.  
 XX  
 KW Histamine H4 receptor; human; antiasmatic; antiallergenic;  
 KM antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 XX diagnosis; gene therapy.  
 OS Homo sapiens.  
 XX  
 PN WO200192485-A1.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 22-FEB-2001; 2001WO-US005914.  
 XX  
 PR 31-MAY-2000; 2000US-0208260P.  
 XX  
 XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX  
 PI Lovenberg T, Liu C;  
 XX  
 DR WPI; 2002-114339/15.  
 XX  
 DR N-PSDB; AAI70980.  
 XX  
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 PS Claim 13; Fig 2; 92pp; English.  
 XX  
 XX The present sequence is that of a human histamine receptor of the H4  
 CC subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA  
 CC library. The invention provides mammalian (human, mouse, rat and guinea  
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the human histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
 CC  
 SQ Sequence 390 AA;  
 Query Match 64.3%; Score 1308.5; DB 5; Length 390;  
 Best Local Similarity 65.1%; Pred. No. 1.9e-128;  
 Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;  
 QY 5 NSTILT-SIKSTIFELSLAIAIMLGWVVIILAFIVRNIRHSNYFELALADPFV 63  
 DB 5 NSTINLSITRYVLAFEMSLVAFALGNALVILAVDKNRHSRYFELALADPFV 64  
 QY 64 GAIAIPLVPSLSLTWTSGKQACVFWLITDYLLCTASVNIIVLISYRQSVSNMVMYA 123  
 DB 65 GVISIFPLVPHLTFEIDPGEKICVFWLITDYLLCTASVNIIVLISYRQSVSNMVMYA 124  
 QY 124 QHSGWKATQWAAVAVIFSFMTNGMILISDSMNSTCECEPGLKKWYFALPTSLLEFL 183  
 DB 125 QHTGVLIKITLWAAVAVLAFVNGPMILVSESKDEGSECEPGEFSEMYILKITSPLFV 184  
 QY 184 ILLIIVAFSAHIYVSIWKREKLSRCLSHVLPSSDSSSDHSHSCQDDPSAATLPARE 243  
 DB 185 IPIILVAFNMNIYWSLWKRDLHSRCQSHPGILTA-VSSNICGHSFGRULSSRSLSASTE 243

QY 244 TTASIGSDKSRKSSILPSIRAYKNSNVIASKMGLSHSDSLALQOREHILFRAKLUAK 303  
 DB 244 VPASFSRQRKSSLSMFSSTRTKMSNTIASMGFSQSDSVLHQRHEVELLRARLAK 303  
 QY 304 SLATILAFATCMAPYSITTYIYISFPFERNLTKSWYHTAFWLOFNSTVNFYPLCHK 363  
 DB 304 SLATILGVFAVCMAPYSITTYIYISFPFERNLTKSWYHTAFWLOFNSTVNFYPLCHK 363  
 QY 364 RFQKAFILKILPVROSTP-PHNRISIT 389  
 DB 364 RFQKAFILKILKQPLPSQHSRVS 390  
 RESULT 11  
 AAG66023  
 ID AAG66023 standard; protein; 390 AA.  
 XX  
 AC AAG66023;  
 XX  
 DT 27-FEB-2002 (first entry)  
 XX  
 DE Human histamine H4 receptor protein.  
 XX  
 KW Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;  
 KW antiasmatic; antiallergic; neuroprotective; antidiabetic; human;  
 KW cerebroprotective; CAMP modulator; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 12..40  
 FT /note= "transmembrane domain"  
 FT Domain 52..69  
 FT /note= "transmembrane domain"  
 FT Domain 88..110  
 FT /note= "transmembrane domain"  
 FT Domain 130..154  
 FT /note= "transmembrane domain"  
 FT Domain 172..196  
 FT /note= "transmembrane domain"  
 FT Domain 304..325  
 FT /note= "transmembrane domain"  
 FT Domain 342..362  
 FT /note= "transmembrane domain"  
 PN WO200185786-A2.  
 XX  
 XX 15-NOV-2001.  
 PD  
 PF 04-MAY-2001; 2001WO-US014527.  
 XX  
 PR 05-MAY-2000; 2000US-0202151P.  
 PR 23-AUG-2000; 2000US-0227567P.  
 PR 13-NOV-2000; 2000US-0247855P.  
 XX  
 PA (AMHP ) AMERICAN HOME PROD CORP.  
 XX  
 PI Jones PG, Blatcher M, Wu S, Pausch MH;  
 XX  
 DR WPI; 2002-049442/06.  
 DR N-PSDB; AAI67750.  
 XX  
 PT New histamine receptor, termed H4 useful for detecting H4 (ant)agonists  
 PT for treating transplanted organ rejection, asthma, allergy, multiple  
 PT sclerosis and rheumatoid arthritis.  
 XX  
 PS Claim 5; Fig 1; 66pp; English.  
 CC The invention provides an isolated histamine receptor, H4, which binds  
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4  
 CC receptor can be expressed by standard recombinant methodology. Cells  
 CC expressing H4 receptor protein at a detectable level can suppress cyclic

CC adenosine monophosphate (cAMP) formation when contacted with the H4  
 CC receptor agonist. The H4 receptor and antibodies are used for identifying  
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful  
 CC for treating transplanted organ rejection, asthma, allergies and  
 CC autoimmune pathologies such as multiple sclerosis, type I diabetes,  
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor  
 CC protein and nucleic acids are useful targets to identify drugs that are  
 CC effective in treating disorders associated with histamine-regulated  
 CC processes. Identification and isolation of H4 receptor provides for  
 CC development of screening of molecules that interact with H4 receptors.  
 CC Genetic variants of H4 can be used to diagnose an H4 associated disease  
 CC as described above. The H4 receptor polynucleotide is useful to treat or  
 CC prevent a disorder associated with the function of H4 in peripheral blood  
 CC leukocytes. The present sequence represents the human histamine H4  
 CC receptor protein

XX Sequence 390 AA;

Query Match 64.3%; Score 1308.5; DB 5; Length 390;  
 Best Local Similarity 65.1%; Pred. No. 1.9e-128;  
 Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-STIKSLTFLMSLAIAMKGNVVIATFVDRNLHRSNYFFLNLAIDFEV 63  
 DB 5 NSTINISLSTRVTLAFEMSLVAFAMIGNALVILAFVDRNLHRSNYFFLNLAIDFEV 64  
 QY 64 GATAIPLTYIPSSLTWTSGKQACVFMILTDTYLLCTASVNVIVISYDRYGSVNAWYRA 123  
 DB 65 GVISITPLTYIPHTLFEWDFGKEICVFMILTDTYLLCTASVNVIVISYDRYGSVNAWYRT 124  
 QY 124 QHSGTWKIATQWAVNIFSFMTNGPMILISDSQNSTTECEPGFLKKYFALPTSLLEFL 183  
 DB 125 QHTGVKITYITLWNAVWVLAFLVNGPMILVSESKWDESECEPFFSWYLAITSFLFEV 184  
 QY 184 IPIILVAVFSAAHIYWSLWKREKLSRCLSHPVLPSSDSSSDHGSRCRDPDSRATLPARKE 243  
 DB 185 IPIILVAVFMNIIYWSLWKRDHLSRCQSHPLTA-VSSNICGHSFRGLSRSSLSASTE 243  
 QY 244 TTASLSDSKRRKSSLLPSIRAYKNSNVIVASKGFLSHSLSLLOQREHLELPARLAK 303  
 DB 244 VPASFSESRORRRKSSLMFSSRTKNSNTIASKMGFSQSDSVLHOREHELLRARRLAK 303  
 QY 304 SLAILLAAPAIICWAPYSLTIVISFPERNLTKSTWHTAFMLQWFSFVNPFLYPLCHK 363  
 DB 304 SLAILLGVPFVCAVPSLFTIVLSFYSSATGPKSVWYRIAFMLQWFSFVNPFLYPLCHK 363  
 QY 364 RFQKAFKLILPVRROSTP-PHNSISIT 389  
 DB 364 RFQKAFKLIFCIKKOPLPSQHSRSVSS 390

RESULT 12

ID AAU74906 standard; protein; 390 AA.

XX AAU74906;

XX 09-APR-2002 (first entry)

XX Amino acid sequence of human G-protein coupled receptor TGR62 protein.

XX Human: G-protein coupled; receptor; GPCR; TGR62; kidney disease;  
 KW signal transduction modulator; cerebral cavernous malformation;  
 KW hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;  
 KW nephritis; hypertension; liver disease; cirrhosis; blood disorder;  
 KW spleen-associated disorder; immune disorder.

OS Homo sapiens.

XX MO200200719-A2.

XX 03-JAN-2002.

XX

PF 25-JUN-2001; 2001MO-US020363.

XX 23-JUN-2000; 2000US-0213461P.

XX (TUL- ) TULARIK INC.

XX Lin DC, Zhao J, Chen J, Cutler G;

DR WPI: 2002-147880/19.

XX N-PSDB; ABK12959.

PT New G-protein coupled receptor polypeptides, useful for identifying  
 PT modulators of signal transduction for treating kidney disease,  
 PT hyperlipidemia, obesity, dyslexia and cardiac myxoma.

PS Claim 26; Page 61; 78pp; English.

XX The present invention relates to a new G-protein coupled receptor (GPCR)  
 CC polypeptide comprising greater than 70% amino acid sequence identity to  
 CC the amino acid sequence of human GPCRs TGR62, TGR21, TGR130.1, TGR130.2,  
 CC human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or  
 CC 90% amino acid sequence identity to human novel edg receptor protein, as  
 CC defined in the specification. The GPCR covalently linked to a solid phase  
 CC is useful for identifying a compound that modulates signal transduction.  
 CC The identified compounds are useful for treating kidney disease, cerebral  
 CC cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac  
 CC myxoma. The molecules of the invention are useful for diagnosing  
 CC disorders or conditions such as kidney-related conditions or diseases  
 CC such as renal failure, nephritis, nephrotic syndrome, asymptomatic  
 CC urinary abnormalities, renal tubule defects, hypertension and  
 CC nephrolithiasis, liver-related disease or condition e.g. cirrhosis,  
 CC infiltrations, lesions, functional disorders and jaundice and spleen-  
 CC associated disorders or conditions e.g. splenic enlargement, immune  
 CC disorders, blood disorders and others. Modulation of the polypeptide of  
 CC the invention is useful to treat or prevent any of the above conditions  
 CC or diseases. The present amino acid sequence represents the human GPCR  
 CC TGR62 protein of the invention. This sequence is one of seven novel G  
 CC protein coupled receptors of the invention (AAU74904- AAU74911)

XX Sequence 390 AA;

Query Match 64.3%; Score 1308.5; DB 5; Length 390;  
 Best Local Similarity 65.1%; Pred. No. 1.9e-128;  
 Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-STIKSLTFLMSLAIAMKGNVVIATFVDRNLHRSNYFFLNLAIDFEV 63  
 DB 5 NSTINISLSTRVTLAFEMSLVAFAMIGNALVILAFVDRNLHRSNYFFLNLAIDFEV 64  
 QY 64 GATAIPLTYIPSSLTWTSGKQACVFMILTDTYLLCTASVNVIVISYDRYGSVNAWYRA 123  
 DB 65 GVISITPLTYIPHTLFEWDFGKEICVFMILTDTYLLCTASVNVIVISYDRYGSVNAWYRT 124  
 QY 124 QHSGTWKIATQWAVNIFSFMTNGPMILISDSQNSTTECEPGFLKKYFALPTSLLEFL 183  
 DB 125 QHTGVKITYITLWNAVWVLAFLVNGPMILVSESKWDESECEPFFSWYLAITSFLFEV 184  
 QY 184 IPIILVAVFSAAHIYWSLWKREKLSRCLSHPVLPSSDSSSDHGSRCRDPDSRATLPARKE 243  
 DB 185 IPIILVAVFMNIIYWSLWKRDHLSRCQSHPLTA-VSSNICGHSFRGLSRSSLSASTE 243  
 QY 244 TTASLSDSKRRKSSLLPSIRAYKNSNVIVASKGFLSHSLSLLOQREHLELPARLAK 303  
 DB 244 VPASFSESRORRRKSSLMFSSRTKNSNTIASKMGFSQSDSVLHOREHELLRARRLAK 303  
 QY 304 SLAILLAAPAIICWAPYSLTIVISFPERNLTKSTWHTAFMLQWFSFVNPFLYPLCHK 363  
 DB 304 SLAILLGVPFVCAVPSLFTIVLSFYSSATGPKSVWYRIAFMLQWFSFVNPFLYPLCHK 363  
 QY 364 RFQKAFKLILPVRROSTP-PHNSISIT 389  
 DB 364 RFQKAFKLIFCIKKOPLPSQHSRSVSS 390

RESULT 13  
 ABG71960  
 ID ABG71960 standard; protein; 390 AA.  
 AC ABG71960;  
 XX  
 XX 28-JAN-2003 (first entry)  
 DE Human G-protein coupled receptor AXOR35.  
 XX  
 XX Human; receptor; G-protein coupled receptor; AXOR35; lymphocyte;  
 KM macrophage; eosinophil; neutrophil; infection; transplant rejection;  
 KM gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;  
 KM Crohn's disease; irritable bowel syndrome; vomiting; inflammation;  
 KM atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;  
 KM psoriasis; urological disease; urinary retention; cardiovascular disease;  
 KM myocardial infarction; hypertension; hypertension; pulmonary disorder;  
 KM chronic obstructive pulmonary disease; cough; renal disease;  
 KM renal ischemia; arteriosclerosis; atherosclerosis; psychosis;  
 KM neurological disorder; migraine; anorexia; anxiety; schizophrenia;  
 KM dyslexia; Parkinson's disease; cancer; obesity; stroke; septic shock;  
 KM grapt versus host disease; osteoporosis.  
 XX Homo sapiens.  
 OS  
 XX US2002137054-A1.  
 PN  
 XX 26-SEP-2002.  
 PD  
 XX 20-JUL-2001; 2001US-00910411.  
 PF  
 XX 02-NOV-1999; 99US-00431898.  
 PR 03-FEB-2000; 2000US-00497790.  
 PR 20-OCT-2000; 2000US-00693761.  
 PA (SMK ) SMITHKLINE BEECHAM CORP.  
 PA (SMK ) SMITHKLINE BEECHAM PLC.  
 PI Aubert KM, Bergema DJ, Fitzgerald L, Graybill TL, Li X;  
 PI Michalovich D, Morrow DM, Zhu Y;  
 DR N-PSDB; ABS57063.  
 DR WPI, 2003-074982/07.  
 XX  
 PT Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for  
 PT treating infections, gastrointestinal disorders, autoimmune disorders,  
 PT urological diseases, cardiovascular diseases and cancer.  
 PS Claim 1; Page 22; 24pp; English.  
 XX  
 XX The invention relates to an isolated G-protein coupled receptor  
 CC polypeptide, AXOR35, (and its homologues, variants, complements and RNA  
 CC polynucleotide (and its homologues, variants, complements and RNA  
 CC equivalents). Also included are an anti-AXOR35 antibody, an AXOR35  
 CC expression vector, producing a recombinant host cell by introducing the  
 CC vector into a cell such that the host cell produces AXOR35, a membrane of  
 CC the host cell expressing AXOR35, identifying/screening for agonists or  
 CC antagonists of AXOR35 and inhibiting or promoting the function of  
 CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,  
 CC by administering to the patient AXOR35 agonists or antagonists. The  
 CC agonist or antagonist identified is useful for treating a disease such as  
 CC asthma, or for inhibiting or promoting the function of lymphocytes,  
 CC macrophages, eosinophils, or neutrophils in diseased tissue such as an  
 CC asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,  
 CC for identifying compounds that are agonists or antagonists of AXOR35, as  
 CC vaccines, or for treating infections (bacterial, fungal, protozoan or  
 CC viral infections), transplant rejection, gastrointestinal disorders (such  
 CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),  
 CC irritable bowel syndrome, vomiting, inflammation (such as atopic  
 CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,  
 CC psoriasis), urological diseases (such as urinary retention),  
 CC cardiovascular diseases (such as myocardial infarction), hypertension,

CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary  
 CC disease), cough, renal diseases (such as renal ischaemia),  
 CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders  
 CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such  
 CC as Parkinson's disease), cancer, obesity, stroke, septic shock, grapt  
 CC versus host disease and osteoporosis. The present sequence represents  
 CC human AXOR35  
 CC  
 XX  
 XX Sequence 390 AA;  
 SQ  
 Query Match 64.3%; Score 1308.5; DB: 6; Length 390;  
 Best Local Similarity 65.1%; Pred. No. 1.9e-126;  
 Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;  
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 DB 5 NSTILMSTRVTLAFPMFLVAFALMLGNALVILAFVDDKILRRSSYFLMLAISDFV 64  
 QY 64 GAIALPLYIPSSLIYWTSGKQCVFMLITDYLLCTASVYNIYLISYDRQSVSNMAYRA 123  
 DB 65 GVISIPLYIPHTLFEMDRGKEICVFMLTDTYLLCTASVYNIYLISYDRYSVSNMAYRT 124  
 QY 124 QHSGTWKATQWVAWVITSPMTNGPMIISDQWQSTCECEGFLKWTYFALPTSLERL 183  
 DB 125 QHTGVAKITVLMVAWVLAFLVNGPMILVBSKQGECEGFSEWYLAITGFLEFV 184  
 QY 184 IPILVAFYSAHIYWSLWKREKLSRCLSHPVLPDSSSDHSGSCRODPDRATIPARKE 243  
 DB 185 IPVILVAFNMNVIYWSLWKRDHLRSQSHPGTLA-VSSNICHSRGRSLRSRSASRE 243  
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 DB 244 VPASFHSERQRKSSLMFSRRTKNNSTIASYMGFSQSDSYALQREHVELLRARLAK 303  
 QY 304 SLATLLAFATCMAPYSLTTVYSPFPERNLTKSTWYHTAFPLQWENSPVNPFLYDLCKK 363  
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 QY 364 RFQKAFKLILPVRRQSTP-PHNRISIST 389  
 DB 364 RFQKAFKLIFCIKQPLPSQHSRSYVS 390  
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 AC ABU92265;  
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 XX 16-JUL-2003 (first entry)  
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 XX Human; receptor; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;  
 KM hARE-5; hRUP3; hRUP5; hRUP6; hRUP7; hGPCR27; hARE-1; hARE-2; hRUP1; hG2A;  
 KM hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUP4; signalling cascade.  
 OS Homo sapiens.  
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 XX US2003017528-A1.  
 PN  
 XX 23-JAN-2003.  
 PD  
 XX 06-JUN-2001; 2001US-00875076.  
 PF  
 XX 20-NOV-1998; 98US-0109213P.  
 PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 28-MAY-1999; 99US-0136435P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.



CC exemplification of the present invention  
XX  
SQ Sequence 390 AA;

SQ Sequence 390 AA;

Query Match	64.3%	Score	1308.5	DB	6	Length	390
Best Local Similarity	65.1%	Pred	No. 1.9e-128				
Matches	252	Conservative	48	Mismatches	84	Indels	3
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[illegible]

Search completed: August 3, 2005, 01:54:03  
Job time : 167 secs



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## ORIGIN

## Alignment Scores:

Pred. No.: 2,426-166 Length: 1451  
Score: 2025.00 Matches: 388  
Percent Similarity: 99.74% Conservative: 0  
Best Local Similarity: 99.74% Mismatches: 1  
Query Match: 99.46% Indels: 0  
DB: Gaps: 0

US-10-626-398-10 (1-389) x AFS58058 (1-1451)

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QY 61 PhePheValGlyAlaIleAlaIleProIeuIleIleProSerSerLeuThrIleThr 80  
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QY 101 ValIleAsnIleValIleIleSerIleAspArgIleGlnSerValSerAsnAlaValIleP 120  
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QY 121 TyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValIlePhe 140  
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QY 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160  
Db 521 TTCTCTTCATCAACAATGGGCGCATGATTCGATTTTCAGACTCTTGCGACAAATGCACT 580  
QY 161 ThrGlnCysGluProGlyPheLeuLysIleTrpIlePheAlaIleuProThrSerLeuLeu 180  
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QY 221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrIleuProAla 240  
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RESULT 2  
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LOCUS  
DEFINITION Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
Nguyen,T., Shapiro,D.A., George,S.R., Setola,V., Lee,D.K.,  
Cheng,R., Rausser,L., Lee,S.P., Lynch,K.R., Roth,B.L. and  
O'Dowd,B.F.  
Discovery of a novel member of the histamine receptor family  
Mol. Pharmacol. 59 (3), 427-433 (2001)

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and  
O'Dowd,B.F.  
Discovery of H4, a Novel Histamine Receptor  
Unpublished  
3 (bases 1 to 1173)

TITLE  
AUTHORS  
O'Dowd,B.F.  
Direct Submission  
Submitted (26-SEP-2000) Pharmacology, University of Toronto, 8  
Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada  
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QY 140 IlePheSerPheMetThrAsnGlyProMetIleleuIleSerAspSerTrpGlnAsnSer 159
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QY 160 ThrThrGluCysGluProGlyPheleuYsleTrpTyrrPheAlaLeuProThrSerleu 179
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QY 240 AlaArgYsleuThrThrAlaSerleuGlySerAspYsleuSerArgYsleuSerleu 259
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DEFINITION Sequence 1 from patent US 6204017.
ACCESSION AR142850
VERSION AR142850.1 GI:15104136
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Umland,S.P. and Wang,S.
TITL Polynucleotide encoding a histamine receptor
JOURNAL Patent: US 6204017-A 1 20-MAR-2001;
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Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
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ACCESSION AR391860  
VERSION AR391860.1 GI:40115588

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1173)  
AUTHORS Behan, J.X., Hedrick, J.A., Laz, T.M., Monema, F.J., Morse, K.L.,  
Umland, S.P., and Wang, S.  
TITLE Histamine receptor  
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;  
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ORIGIN  
US-10-626-398-10 (1-389) x AR391860 (1-1173)

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Score: 1308.50 Matches: 252  
Percent Similarity: 77.52% Conservative: 48  
Best Local Similarity: 65.12% Mismatches: 84  
Query Match: 64.27% Indels: 3  
Gaps: 3

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Db 373 CAACATCTAGGGGCTCTTGAAGATGTTACTGATGCTGAGCGGCTTGGGCTGCGCTTC 432  
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTyrGlnAsnSerThrGlnGlyCys 163  
Db 433 TTAGTGAATGGGCGCAATGATTTCTAGTTCAAGATCTTGAAGATGATGATGATGATGAT 492  
Qy 164 GluProGlyPheLeuIleTyrTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183  
Db 493 GAACCTGATTTTTCGGAATGGTACATCTTGCATCATCATCATCATCATCATCATCATCAT 552  
Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTyrSerIleuThrIleVal 203  
Db 553 ATCCAGATCATCTGTGCTGCTTATTCATGATGATGATGATGATGATGATGATGATGATGAT 612  
Qy 204 GluTyrLeuSerArgCysLeuSerHisProValIleProSerAspSerSerSerAsp 223  
Db 613 GATCATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669  
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgIleGlu 243  
Db 670 TGTGACACTCATCTTCAAGTAGACTACTCTTCAAGAGATCTTCTTCATCGACAGAA 729

QY	244	ThrlrhllasleSleuGLySerAspIySerIargIySerserSleuLeuProSerIle	263
Db	730	GTTCCTGCATCCTTTCAATTCAGAGACAGAGAGAAAGAGTCTATGCTTTTCTTCA	789
QY	264	ArgAlaTrYLyAsnSerAsnValIlealaserIySmecIyPheLeuSerHisSerAsp	283
Db	790	AGAACCAAGATGATAGCATATACATATTCCTCCAAATAGGGTCTCTTCCCAATACAT	849
QY	284	SerleuAlaLeuGlnGlnIargGluHisIleGluLeuPheAlaIargIyLeuAlaIys	303
Db	850	TCTGTAGCTCTTCCAAAGGAGACATGTGAACGCTTAAGACGACAGATTAAGCCAAAG	909
QY	304	SerleuAlaIleLeuLeuAlaAlaPheAlaIleCySTrpAlaProIySerIeuThrThr	323
Db	910	TCACGTGGCATCTCTTACGAGGCTTTTCTGTCTCTGCGCTCATATTCCTGTTCACA	969
QY	324	ValIeTrYSerPhePheProGluIargAsnLeuThIySserThrTrpTyHieThrla	343
Db	970	ATTTGCTTTATTTTATTTCTCTCAGCAACAGTCCCTAATACATGTTGGTATAGATTTCA	1029
QY	344	PheTrIleuGlnItrPheAsnSerPheValaAsnProPheLeuTyPProIeuCyHisIys	363
Db	1030	TTTGGCTTCAGTGTTCAATTCCTTTGTCAACCTCTTTGTATCCATGTGTACAAAG	1089
QY	364	ArgPheGlnIyAlaPheLeuIyIleLeuProValArgArgIlnSerThrPro---Pro	382
Db	1090	CGCTTTCAAAAGGCTTTCTTGAAATATTTGTATATAAAAAAGCAACCTTACCATCACAA	1149
QY	383	HisAsnArgSerIleSerThr	389
Db	1150	CACAGTCGGTCAGTATCTTCT	1170

LOCUS	AX109119	1173 bp	DNA	linear	PAT 30-APR-2001
DEFINITION	Sequence 1 from Patent WO0125432.				
ACCESSION	AX109119				
VERSION	AX109119.1	GI:13924093			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L., Umland, S., and Wang, S.				
TITLE	Histamine receptor				
JOURNAL	Patent: WO 0125432-A 1 12-APR-2001; SCHERING CORPORATION (US)				
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Alignment Scores:					
Pred. No.:	3,62e-104	Length:	1173		
Score:	1308.50	Matches:	252		
Percent Similarity:	77.52%	Conservative:	48		
Best Local Similarity:	65.12%	Mismatches:	84		
Query Match:	64.27%	Indels:	3		
	6	Gaps:	3		
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QY	24 LeuAlaIleAlaIleMerLeuGlyAenValValIleLeuAlaPheIleValAspArg	43			
Db	73 GTAGCTTTTGCTATATATCTGGAAATCTTGTCATTTTAGCTTTGTGTGTCAGAA	132			

Oy	44	AsnLeuNtrghIsaGSeSerAsnTyRPhheLeuNleuMaIaIeAlaAaRPhheNeI	63
Db	133	AAcCTTGAACATCGAAGATGATATTTTTCCTTAACCTGGCCATCTCGACTTCCTTGTG	192
Oy	64	GIyAlaIaIeAlaIeProLeuTyRlIeProSeSerLeuThrTyRTPThSeGlyLys	83
Db	193	GGTGATCTTCATTCCTTCCTTGTACATCCCTCACAAGCTGCTTCGAATGGGATTTTGGAAAG	252
Oy	84	GIaIaIaCyValaPheTPLeuIleThraAPTyRLeuLeuCyStrhAlaSeValTyRAsn	103
Db	253	GAATTCGTGATATTTTGGCTCAGACATGACATATCGTATGTATGATACAGATCTGATATATAC	312
Oy	104	IlleValleuIleSeTyRAspATyRGlInSeValSerAsnAlaValTyRPyRAla	123
Db	313	ATTGTCCCATCAGACTATGATCGATACCTGTGCAAGTCCMAATGCTGTCTTAAGAAGCT	372
Oy	124	GIhIaSeSerGlyThrTPLeuIleAlaAlaThrcGlInMetValAlaValTPRlIePheSerPhe	143
Db	373	CAACATATGGGGTCTTGAAATGTTACTGTGATGGGGCCGTTGGTGGCTTC	432
Oy	144	MetThraNglPyRometIleLeuIleSezAspSerTPGInAsnSeThrThcGlInCys	163
Db	433	TTATGTGATGGCCCAATGATCTCTGATTTCAAGCTTGGAAAGATGAAGATGAAGT	492
Oy	164	GIuDPrgIyPheLeuLysTyRTPyRPhaIaLeuProThrSerLeuLeuGIuPheLeu	183
Db	493	GAACCTGATATTTTTCGGAAATGGTATACCTTCCTCCATCATCATATCTTGGAAATTCGTG	552
Oy	184	IlleProIleLeuLeuValAlaTyRPheserAlaIleTyRTPRserLeuTPRlyAspG	203
Db	553	ATCCAGCATCTTATGCTTATTTTCAACATGAATATTTTATGAGCTGTGAAAGGT	612
Oy	204	GIuLyLeuSeSerATyCySeLeuSerHlProValIleuProSezAspSeSerSezAsp	223
Db	613	GATCATCTCGATAGCTGACCAAGCAAGCATCTTGACTGACTGCT---GTCTTCCAAATC	669
Oy	224	HisGIyHlSeSerCyVarGInAspProAspSerAlaThrIleuProAlaGlyLeu	243
Db	670	TGTGAGACCTCATTCAGAGTAACTATCTTCAAGAGATCTCTTTCGATCCGACAGAA	729
Oy	244	ThrThraIaSeSerLeuGlySeSerAspLysSerTgATgLySeSerLeuLeuProSerIle	263
Db	730	GTTCCTGCTATCTTTCATTCAGAAAGACAGAGGAGAAAGATGATCTCATGTTTCCSCA	789
Oy	264	ArgAlaTyRlyAsnSeSerAsnValIleAlaSerLySmetGIyPheLeuSezHlSezAsp	283
Db	790	AGAACAAGATGAATGACAAATACATATGCTTCCAAATGGTCTCTTCCCAATCAGAT	849
Oy	284	SeTleuAlaLeuGInGInATgIuHlIeGlyIleuPheAlaGAlaGlyLysLeuAlaLys	303
Db	850	TCGTAGCTTTCACCAAGGGAGAAATGTTGAATCGCTTAAGCAGAGATTTGCCCAAG	909
Oy	304	SeTleuAlaIleLeuLeuAlaIaIaPheAlaIleCyStrAlaProTyRSeLeuThrThr	323
Db	910	TCACGTGGCATCTTCTTAAGGGTGTTCGTTCGTGGCTGCATATTCCTGTGTCA	969
Oy	324	ValIleTyRSeRPhheProGluAlaGAsnLeuHlLysSeThrTPRtyHlIeThraIa	343
Db	970	ATTGTCTTATATTTATTTCTCAGCAACAGCTCTAAATATGATGGTATGAATTTCA	1022
Oy	344	PheTPRLeuGInTPRPhaSeSerPheValaAsnProPheLeuTyRProLeuCyHlIaLys	363
Db	1030	TTTTGGCTTCAGTGTTCATATCTCTTGTCAATCTCTTTGTATCCATGTGTGTACAAG	1088
Oy	364	ArgPheGInLyAlaPheLeuLysIleLeuProValaArgATGInSeThrPro--Pro	382
Db	1090	CGCTTTCAAAAGGCTTCTTGAATAATATTTGTATTAATAAAGCAACCTTCACATCAGAA	1149
Oy	383	HisAsnAspSerIleSeThr 389	
Db	1150	CACAGTCGCTAGTATCTCT 1170	

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RESULT 6
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LOCUS             Sequence 1 from Patent EP1096009.
DEFINITION        AX139113
ACCESSION         AX139113
VERSION           AX139113.1 GI:14274791
KEYWORDS
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1
AUTHORS           Peter, B. and O'Reilly, M.A.
TITLE             G-protein coupled receptor-like polypeptide
JOURNAL           Patent: EP 1096009-A 1 02-MAY-2001;
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Alignment Scores:
Pred. No.:        3,62e-104      Length:      1173
Score:            1308.50        Matches:     252
Percent Similarity: 77.52%      Conservative: 48
Best Local Similarity: 65.12%   Mismatches:  84
Query Match:      64.27%        Indels:       3
DB:               Gaps:         3
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QY      24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
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DB      133 AACCTTAGCATCGAAGTAGTATTTTCTTAACTTGCCATCTGACATCTTCTTGTG 192
QY      64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
DB      193 GGTGTCATCTCCATTCCTTTGTCATCCCTCACACGCTGTCGATGCGATTTTGAAG 252
QY      84 GlnAlaCysValPheIlePheLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
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QY      433 TTAGTCAATGGGCGCATGATTTCTAGTTTCAGAGCTTTGGAAGAGATGAAGTAGTATGT 492
QY      144 MetThrAsnGlyProMetIleLeuIleSerAspSerTyrGlnAsnSerThrThrGlyCys 163
DB      493 GAACCTGGATTTTTCGGAATGTCATCTTGCCATCACATCATCTTGGATTTGCGT 552
QY      164 GluProGlyPheLeuLysTyrTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
DB      493 GAACCTGGATTTTTCGGAATGTCATCTTGCCATCACATCATCTTGGATTTGCGT 552
QY      184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTyrPheAsp 203
DB      553 ATCCGAGTCACTTACGCTTATTTTCAACATGATATTTATTGAGAGCTGTCGAGAGCT 612
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QY      204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB      613 GATCATCTCAGTAGGTGCGCAAGCCATCTGAGTACTGCT---GTCTCTTCAACATC 669
QY      224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
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DB      790 AGAACCAAGATGAATAGCAATTCATTCCTTCAAAATGCGTCTCTCCCAATCAGAT 849
QY      284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB      850 TCTGTAGCTCTTCAACCAAGGAGACATGTGAACTGCTTAGGCCAGAGATTTAGCCAA 909
QY      304 SerLeuAlaIleLeuLeuAlaIleAlaPheAlaIleCysTyrAlaProTyrSerLeuThrThr 323
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QY      389 HisAsnArgSerIleSerThr 389
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LOCUS             Sequence 1 from Patent WO0185786.
DEFINITION        AX301763
ACCESSION         AX301763
VERSION           AX301763.1 GI:17382844
KEYWORDS
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
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                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1
AUTHORS           Jones, P.G., Blatcher, M., Wu, S. and Pausch, M.H.
TITLE             Human histamine h4r receptor
JOURNAL           Patent: WO 0185786-A 1 15-NOV-2001;
                  American Home Products Corporation
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Alignment Scores:
Pred. No.:        3,62e-104      Length:      1173
Score:            1308.50        Matches:     252
Percent Similarity: 77.52%      Conservative: 48
Best Local Similarity: 65.12%   Mismatches:  84
Query Match:      64.27%        Indels:       3
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US-10-626-398-10 (1-389) x AX301763 (1-1173)
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QY 24 LeuAlaIleAlaIleMetLeuGlyAenValValIleLeuAlaPheIleValaParg 43
DB 73 GTAGCTTTTGCTATATGCTAGGAAATGCTTGTGCTATTTAGCTTTTGCGTGACAA 132
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DB 133 AACCTTAGACATCGAAGTAGATATTTTCTTAACCTTGCCATCTGACCTTCTTG 192
QY 64 GAlaAlaIleAlaIleProLeuTyrIleProSerSerIleuThrTyrTrpThrSerGlyLys 83
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QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgYsGlu 243
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QY 244 ThrThrAlaSerLeuGlySerAspYsSerArgArgYsSerSerLeuProSerIle 263
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LOCUS BD015847
DEFINITION Novel polypeptide.
ACCESSION BD015847
VERSION BD015847.1 GI:2256984
KEYWORDS JP 2001211889-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Peter, B. and Olaylee, M.A.
TITLE Novel polypeptide
JOURNAL Patent: JP 2001211889-A 1 07-AUG-2001;
PUBLISHER INC
OS Homo sapiens (human)
PN JP 2001211889-A/1
PD 07-AUG-2001
PF 27-OCT-2000 JP 2000329359
PR 29-OCT-1999 GB 9925641.4, 20-APR-2000 GB 0009973:9 PI
BEAT PETER, MARK ANTONY OLAYLEE
PC C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P1/04,
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Pred. No.: 3,62e-104 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
Gaps: 3
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QY 44 AenLeuArgHisArgSerAntyrPhePheLeuAenLeuAlaIleAlaPhePheVal 63
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Oy      324 ValIleTyrSerPhePheProGluArgAsnLeuThrIleSerThrTyrTyrHisThrAla 343
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RESULT 9
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LOCUS      Homo sapiens histamine H4 receptor mRNA, complete cds.
DEFINITION      AF307973
ACCESSION      AF307973.1 GI:11141732
VERSION

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KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE      Jones, P.G., Wu, S. and Betty, M.
      1 (bases 1 to 1173)
      Cloning of a novel histamine receptor
      Unpublished
      2 (bases 1 to 1173)
      Jones, P.G., Wu, S. and Betty, M.
      Direct Submission
      Submitted (25-SEP-2000) Neuroscience, Wyeth Ayerst, CN8000,
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Pred. No.:      3,62e-104      Length:      1173
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Best Local Similarity:      65.12%      Mismatches:      84
Query Match:      64.27%      Indels:      3
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Oy      104 ILevalIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrPyrAla 123
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Oy		383	HisAsnArgSerIleSerThr	389
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LOCUS		1173 bp	mRNA	linear PRI 11-SEP-2001
DEFINITION				
ACCESSION		AF325356		mRNA, complete cds.
VERSION				
KEYWORDS		AF325356.1 GI:15553202		
SOURCE				
ORGANISM		Homo sapiens (human)		
AUTHORS		Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1173)		
REFERENCE		Zhu,Y., Michalovich,D., Wu,H.-L., Tan,K.B., Dycko,G.M., Mannan,I.J., Boyce,R., Alston,J., Tierney,L.A., Li,X., Herley,N.C., Vawter,L., Sarau,H.M., Ames,R.S., Davenport,C.M., Hibbe,P., Wilson,S., Bergma,D.J. and Fitzgerald,L.R. Cloning, expression, and pharmacological characterization of a novel human histamine receptor		
JOURNAL MEDLINE PUBMED		Mol. Pharmacol. 59 (3), 434-441 (2001) 21106320 11179436		

REFERENCE 2 (bases 1 to 1173)  
AUTHORS Zhu,Y., Michalovich,D. and Fitzgerald,L.R.  
TITLE Direct Submission  
JOURNAL Submitted (30-NOV-2000) GlaxoSmithKline, 709 Swedeland Rd., PO Box 1539, King of Prussia, PA 19406, USA

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ORIGIN

Alignment Scores:  
Pred. No.: 3.62e-104 Length: 1173  
Score: 1308.50 Matches: 252  
Percent Similarity: 77.52% Conservative: 48  
Best Local Similarity: 65.12% Mismatches: 84  
Query Match: 64.27% Indels: 3  
DB: 9 Gaps: 3

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ACCESSION AF329449  
VERSION AF329449.1 GI:13876643  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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More, K.L., Behan, J., Laz, T.M., West, R.E., Jr., Greenfeder, S.A.,  
Antnes, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shih, N.,  
Gustafsson, S.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.,  
and Monsma, F.J., Jr.  
Cloning and characterization of a novel human histamine receptor  
J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)  
TITLE JOURNAL  
MEDLINE 21104636  
PUBMED 1181941  
2 (bases 1 to 1173)  
Monsma, F.J., Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and  
Bayne, M.  
Direct Submission  
Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough  
Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,  
USA

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ORIGIN  
Alignment Scores:  
Pred. No.: 3,62e-104 Length: 1173  
Score: 1308.50 Matches: 252  
Percent Similarity: 77.52% Conservative: 48  
Best Local Similarity: 65.12% Mismatches: 84  
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ACCESSION      AY136745
VERSION      AY136745.1 GI:22658472
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ORGANISM      Homo sapiens
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            Direct Submission
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ORIGIN
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Pred. No.: 3,62e-104 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 9 Gaps: 3
US-10-626-398-10 (1-389) x AY136745 (1-1173)

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Qy      64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTyrPheSerGlyLys 83
Db      193 GGTGATATCCATTCCTTTGTATCATCCCTCACACGCTGTGCAATGGGATTTTGAAG 252
Qy      84 GlnAlaCysValPheThrLeuIleThrAaspTyrLeuLeuCysThrAlaSerValTyrAsn 103
Db      253 GAATGTGTATATTTTGGCTCACTAGTACTGATCTGTATGTAACAGATGTATATAC 312
Qy      104 IleValLeuIleSerTyrAaspArgTyrGlnSerValSerAanAlaValTyrArgAla 123
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Qy      124 GlnHisSerGlyThrTyrPheLysIleAlaThrGlnMetValAlaValTyrPheSerPhe 143
Db      373 CAACATACGTGGGTCTTGAAGATGTACTGTATGATGATGATGATGATGATGATGATGAT 432
Qy      144 MetThrAanGlyProMetIleLeuIleSerAapSerThrProIleAanSerThrGluCys 163
Db      433 TTAGTAAATGGCCATGATGATTTCTAGTTTCAAGATCTTGAAGATGAGTATGATGT 492
Qy      164 GluProGlyPheLeuLysTyrTyrPheAlaLeuProThrSerLeuGlnPheLeu 183
Db      493 GAACCTGATTTTTCGGAATGTATCATCTCCATCATCATCATCTTGAATTCGTG 552
Qy      184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTyrPheSerLeuTyrPheArg 203
Db      553 ATCCAGATCATCTTATGCTTATTTTCAACATGAATATTAATGAGCCGTGGAAGCGT 612
Qy      204 GlyLysLeuSerArgCysLeuSerHisProValIleProSerAapSerSerSerAap 223
Db      613 GATCATCTCAGTAGTCGCAAGGCATCTCGACTGCTCTCTCCACATC 669
Qy      224 HieGlyHisSerCysArgGlnAaspProAaspSerArgAlaThrLeuProAlaArgLyGlu 243
Db      670 TGTGACACTCATCTCAGAGTAGACTATCTTCAAGGAGATCTCTTGTGATGACAGAA 729
Qy      244 ThrThrAlaSerLeuGlySerAapLySerArgArgLySerSerLeuLeuProSerIle 263
Db      730 GTTCCGACATCTTCTTCACTCAGAGACAGAGAGAAAGTAGTGTCTCATGTTTCTCTCA 789
Qy      264 ArgAlaTyrLeuAenSerAenValIleAlaSerLyMetClyPheLeuSerHisSerAap 283
Db      790 AGAACCAAGATGATAGCAATACATTCCTTCCAAATGGCTCTTCTCCCATCATCAT 849
Qy      284 SerLeuAlaLeuGlnGlnArgGluHisIleGlyLeuPheArgAlaArgLySleuAlaLys 303
Db      850 TCTGTAGCTCTTCAACCAAGGAAACATGTTGAACTGTTAGCGCAGAGAAATTAGCCAA 909

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QY 304 SerLeuAlaIleLeuLeuAlaIaIaPheAlaIleCyStrPaIaProTyrSerLeuThr 323  
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QY 324 ValIleTyrSerPhePheProGluArgAnLeuThrLysSerThrTrpTyrHisThrAla 343  
DB 970 ATGTCCTTCATTTTATTCCTCAGCACACAGGCTCTAAATCATTTGGATAGAAATTGCA 1029  
QY 344 PheTrpLeuGlnTrpPheAnSerPheValAnProPheLeuTyrProLeuGlyHisLys 363  
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QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro--Pro 382  
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QY 383 HisAnArgSerTyrLysSerThr 389  
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RESULT 13  
HSA298292 1173 bp mRNA linear PRI 12-JAN-2002  
LOCUS HSA298292 Homo sapiens mRNA for histamine receptor H4 (HRH4 gene).  
DEFINITION AJ298292  
VERSION AJ298292.1 GI:18152452  
KEYWORDS histamine receptor H4; HRH4 gene.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 O'Reilly M.A.  
AUTHORS Identification of a histamine H4 receptor on human eosinophils -  
TITLE Role in eosinophil chemotaxis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1173)  
AUTHORS O'Reilly M.A.  
TITLE Direct Submision  
JOURNAL Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer  
Ltd, Ramsgate Road, Sandwich, Kent, CT13 9NU, UNITED KINGDOM

FEATURES  
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ORIGIN  
Alignment Scores:  
Pred. No.: 3 62e-104 Length: 1173  
Score: 1308.50 Matches: 252  
Percent Similarity: 77.52% Conservative: 48

Best Local Similarity: 65.12% Mismatches: 84  
Query Match: 64.27% Indels: 3  
DB: 9 Gaps: 3  
US-10-626-398-10 (1-389) x HSA298292 (1-1173)

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QY 24 LeuAlaIleAlaIleMetLeuGlyAnValValIleLeuAlaPheIleValAspArg 43  
DB 73 GTAGCTTTGCTATATATCTAGAAATCTTGGTCATTTTATGCTTTGCTGTCGACAA 132  
QY 44 AenLeuARGHSARGSerAnTyrPhePheLeuAnLeuAlaIleAlaAspPheVal 63  
DB 133 AACCTTAACATCGAAGTAGTATTTTCTTAATCTGGCCATCTGACTCTTTGTG 192  
QY 64 GYAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83  
DB 193 GGTGTGATCTCATTCCTTGGGCTTGTACATCCCTCAGACGCTGTTGAAATGGGATTTGGAAAG 252  
QY 84 GlnAlaCyValPheTrpLeuIleThrAspTyrLeuLeuCyStrPaIaSerValTyrAn 103  
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QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143  
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QY 144 MetThrAnGlyProMetIleLeuIleSerAspSerTrpGlnAnSerThrTrpGlyCys 163  
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QY 164 GluProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183  
DB 493 GAACCTGATTTTTTTCGGAATGATGATACCTTGCCATCACAATCTTGGAAATTCGCG 552  
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203  
DB 553 ATCCAGATCATCTAGTCGCTTATTCAACATGAAATATTATTAGAGCTGTGAAGCGT 612  
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223  
DB 613 GATCATCTCAGTAGGTGCCAAGCCATCTGACGACTGCT--GTCCTTCCCAACATC 669  
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243  
DB 670 TGTGACACTCATTTAGAGGTAGACTATCTTACAGAGATCTCTTCTGATCAGACAGA 729  
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263  
DB 720 GTTCTCGATCTCTTCATTCAGAGAGACAGAGAGAAAGATGATCTCATGTTTCTCA 789  
QY 264 ArgAlaTyrLysAnSerAnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283  
DB 790 AGAACCAAGATGAATAGAAATACATTCCTTCCAAATGGGTCTCTCCCAATCCAGAT 849  
QY 284 SerLeuAlaLeuGlnGluArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303  
DB 850 TTGTAGCTCTTACCAAGGAAACATGTTAACTGCTTAGAGCCAGAGATTAAGCCAG 909  
QY 304 SerLeuAlaIleLeuLeuAlaIaPheAlaIleCyStrPaIaProTyrSerLeuThrTrp 323  
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QY 324 ValIleTyrSerPhePheProGluArgAnLeuThrLysSerThrTrpTyrHisThrAla 343  
DB 970 ATGTCCTTCATTTTATTCCTCAGCAACAGGCTCTAAATCAGTTTGTATAGAAATTGCA 1029

QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrrProLeuCySHisIlys 363  
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QY 383 HisAsnArgSerIleSerThr 389  
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RESULT 14  
AX376577 1266 bp DNA linear PAT 01-MAR-2002  
LOCUS AX376577  
DEFINITION Sequence 5 from Patent WO0200719.  
ACCESSION AX376577  
VERSION AX376577.1 GI:19170678  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 Lin, D.C., Zhao, J., Chen, J.L. and Cutler, G.  
AUTHORS Novel receptors  
TITLE Patent: WO 0200719-A 5 03-JAN-2002;  
JOURNAL Tularik Inc. (US)

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VSNICGHSRGRGLSSRRSLASTVEYSPHSRORRKSLSMSSTTKNSNTIASKM  
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ORIGIN  
Alignment Scores:  
Pred. No.: 4.02e-104 Length: 1266  
Score: 1308.50 Matches: 252  
Percent Similarity: 77.52% Conservative: 48  
Best Local Similarity: 65.12% Mismatches: 84  
Query Match: 64.27% Indels: 3  
Gaps: 3  
US-10-626-398-10 (1-389) x AX376577 (1-1266)

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QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValIleValIleLeuAlaPheIleValaParg 43  
Db 97 GTAGCTTTTGCTTAATGTCTAGGAAATGTCTTGCTCTTTTACCTTTTGCTGTCGACAA 156  
QY 44 AsnLeuArgHisArgSerAsnTyrrPhePheLeuAsnLeuAlaIleAlaPhePheVal 63  
Db 157 AACCTTAGACATGCAAGTACTTATTTTCTTAACCTTGCCATCTGCTCTTATG 216  
QY 64 GlyAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrTrpThrSerGlyIys 83

Db 217 GGTGATGATCCATTCCTTTGTACATCCCTCACAGCCTGTTGCATAGGATTTGGAAAG 276  
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrrLeuIleCysThrIleAsnValIleAsn 103  
Db 277 GAATGCTGATATTTGGCTCAGTACATCTGTATGATACACATCTGTATATAC 336  
QY 104 IleValIleIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaValTyrrIleGAla 123  
Db 337 ATGTGCTCATCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 396  
QY 124 GlnHisSerGlyThrTyrrIleAlaIleThrGlnMetValIleValIlePheSerPhe 143  
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QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGlyCys 163  
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Db 577 ATCCAGATCATCTTATGCTGCTTATTTCAACATGATATTTATTTGAGACCTGTGGAAGCGT 636  
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QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrIleProAlaArgGlyGln 243  
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QY 244 ThrThrIleSerLeuGlySerAspIysSerArgArgIysSerSerLeuLeuProSerIle 263  
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QY 304 SerLeuAlaIleLeuLeuAlaIleAlaPheAlaIleCysTrpAlaProTyrrSerLeuThr 323  
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QY 324 ValIleTyrrSerPhePheProGluArgAsnLeuThrIysSerThrTyrrTyrrHisThrAla 343  
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Db 1054 TTTGGCTTCAGAGGCTTCATTCCTTGTGCAATCCTTTGTATTCATTGTGTGCACAG 1113  
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QY 383 HisAsnArgSerIleSerThr 389  
Db 1174 CACAGTCGGTCAGATCTTCT 1194

RESULT 15  
AX301229 1300 bp DNA linear PAT 30-NOV-2001  
LOCUS AX301229  
DEFINITION Sequence 1 from Patent WO0185793.  
ACCESSION AX301229  
VERSION AX301229.1 GI:17382320  
KEYWORDS



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 17:49:01 ; Search time 573 Seconds  
(without alignments)  
4018.812 Million cell updates/sec

Title: US-10-626-398-10  
Perfect score: 2036  
Sequence: 1 MANNSTALTSIKISLTL.....LKLPRRQSTPPHNRISST 389

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 segs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seg length: 0  
Maximum DB seg length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2025	99.5	1170	6	AA170983 Guinea pi
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5	1308.5	64.3	1173	4	AA083203 Human GPC

6	1308.5	64.3	1173	5	AAH24007	AAH24007 Human G p
7	1308.5	64.3	1173	6	ABZ80663	ABZ80663 Human his
8	1308.5	64.3	1173	6	ABQ78739	ABQ78739 Nucleocid
9	1308.5	64.3	1173	6	AA170980	AA170980 Human his
10	1308.5	64.3	1173	6	AA167750	AA167750 Human his
11	1308.5	64.3	1173	8	ACA93262	ACA93262 Human cdn
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15	1308.5	64.3	1173	12	ADG86374	ADG86374 Human end
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18	1308.5	64.3	1173	12	ADQ75073	ADQ75073 Human cdn
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24	1308.5	64.3	3689	12	ADO29967	ADO29967 Human GPC
25	1306.5	64.2	1227	4	AA166009	AA166009 Human GPR
26	1306.5	64.2	1265	6	AA598078	AA598078 Human DNA
27	1306.5	64.2	1265	6	AA055125	AA055125 Human H4
28	1244	61.1	1176	6	AA170981	AA170981 Mouse his
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30	1235.5	60.7	1176	6	AA170982	AA170982 Rat hist
31	1166	57.3	1166	9	AA055124	AA055124 Human H4
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34	694.5	34.1	1239	3	AAA70639	AAA70639 Rat G-pro
35	694.5	34.1	2700	3	AAA70640	AAA70640 Rat G-pro
36	693.5	34.1	2700	2	AAH44571	AAH44571 G-protein
37	689.5	33.9	1334	2	AAH44573	AAH44573 Human mus
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39	689.5	33.9	1335	3	AAH09062	AAH09062 Human his
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43	689.5	33.9	1335	13	ADR31457	ADR31457 Human his
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## ALIGNMENTS

RESULT 1	AA170983	standard; cDNA; 1170 BP.
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AC	AA170983;	
XX		
DT	18-MAR-2002 (first entry)	
XX		
DE	Guinea pig histamine H4 receptor cDNA.	
XX		
KW	Histamine H4 receptor; guinea pig; antiasthmatic; antiallergenic; antiinflammatory; cardiact; circulatory; antidiabetic; laxative; diagnosis; gene therapy; ss.	
XX		
OS	Cavia porcellus.	
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PN	WO200192485-A1.	
XX		
PD	06-DEC-2001.	
XX		
PF	22-FEB-2001; 2001WO-US005914.	
XX		
PR	31-MAY-2000; 2000US-0208260P.	
XX		
PA	(ORTH ) ORTHO-MCNEIL PHARM. INC.	
XX		
PI	Lovenberg T, Liu C;	
XX		
DR	WPI; 2002-114339/15.	

DR P-PSDB; AAM50567.

XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
PT the proteins, useful in gene therapy for treating diseases where it is  
PT beneficial to elevate mammalian histamine H4 receptor activity.

PS Claim 4, Fig 6B, 92pp, English.

XX The present sequence is that of a cDNA clone encoding guinea pig  
CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone  
CC marrow cDNA library. It shows 75.6% homology to the human H4 receptor  
CC coding region. The invention provides mammalian (human, mouse, rat and  
CC guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-  
CC 83) and polypeptides (see AAM50564-67). The nucleic acids have been  
CC expressed in recombinant host cells that produce active recombinant  
CC protein. The pharmacology of known histamine ligands is demonstrated.

CC Mammalian histamine H4 receptor may be used in gene therapy for the  
CC treatment of diseases where it is beneficial to elevate mammalian  
CC histamine H4 receptor activity. Recombinant protein is useful for  
CC identifying modulators of the mammalian histamine H4 receptor. Such  
CC modulators may be useful for diagnosing, treating or preventing asthma,  
CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-  
CC insulin dependent diabetes mellitus, hyperglycemia, constipation,  
CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity

XX Sequence 1170 BP; 301 A; 286 C; 221 G; 362 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,14e-189 Length: 1170

Score: 2025.00 Matches: 388

Percent Similarity: 99.74% Conservative: 0

Best Local Similarity: 99.74% Mismatches: 1

Query Match: 99.46% Indels: 0

DB: 6 Gaps: 0

US-10-626-398-10 (1-389) x AAI70983 (1-1170)

QY 1 MetLeuAlaAsnAsnSerThrIleAlaLeuThrSerIleLeuSeriLeuThrPheLeu 20  
DB 1 ATGTGGCAAAATTAACAGTACATCCCTTAACATCAATTAATTTCTTGACATTTTAA 60  
QY 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValAlaValIleLeuAlaPheIle 40  
DB 61 ATGCTTTACTAGCTAATGCTATTAATGTTAGGCAATGCTGGTCAATTTTACCTTTTAT 120  
QY 41 ValaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAsp 60  
DB 121 GTGGACAGAAATCTTAGCATGGAATTAATCTTTTCTTAACCTTGCCCTTGCAAC 180  
QY 61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80  
DB 181 TTCTTTGTGGGTGCAATGCAATTCCTCTGTACATACCTTCCTGCTGACTTACGAGACT 240  
QY 81 SerGlyValGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100  
DB 241 TCTGAAAGCAAGCTGTGTATTTTGGCCATTAAGTACTTCTTTTATGACAGCACTT 300  
QY 101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrp 120  
DB 301 GGTATTAATATTGCTCTCATGCTACGATCCGTCACGATCGTCAATGCCGTGTGG 360  
QY 121 TyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIle 140  
DB 361 TATAAGCTCAGCACTGCTGCACTGAAATTTGCTACTCAGATGCTGCTTTGGATA 420  
QY 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160  
DB 421 TTCTCTTCATGACAAATGGCGCATGATTCGATTTTCAAGCTCTTGGCAGAAATGCACT 480  
QY 161 ThrGlnCysGlnProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeu 180  
DB 481 ACAGATATGGAACCTGATTTTAAAGAGTGTAATTTGCTCTCTCCATCATCATTAATTG 540

QY 181 GluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200  
DB 541 GAATTCCTGATCCCATCTTGTAGTCTTATTATTCAGCGCCCATATTATTCAGAGCTGG 600  
QY 201 TrpLysArgGlyLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220  
DB 601 TGGAGCGAGAAACCTGAGAGGTGCTGAGCCACCTGTATCTCCCTTGATCTCTTCC 660  
QY 221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240  
DB 661 AGCATGACCAAGACATCTCTGACAGACAGACCCGATTCAGAGGCACTTGCACACA 720  
QY 241 ArgLysGlnThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeu 260  
DB 721 CGGAAGAAACAACGCTCTCTTGTTCAAGCAAGTCACGGAGAAAGAGCAGTCTTGG 780  
QY 261 ProSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSer 280  
DB 781 TTTTCCATMAAGCTTACMAAGACGCAATGTGATCGGTTCCMAAATGGCTTCTCTCC 840  
QY 281 HisSerAspSerLeuAlaLeuGlnGlnArgGlnHisIleGlnLeuPheArgAlaArgLys 300  
DB 841 CACTCAGATTCCTTGCTCTCTTCAAGAAAGGAAACATATCGAATTTTCAAGCCAGAAA 900  
QY 301 LeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSer 320  
DB 901 TTAGCCAAAGTACATGGCCATCACTTACAGACTTTTGCCATTTGCTGGGCTTCATATCA 960  
QY 321 LeuThrTrpValIleTyrSerPhePheProGlnArgAsnLeuThrLysSerThrTrpTyr 340  
DB 961 CTGATACAGATTAATCTCAATTTTCTTGAAGAACTTGAATCAACTGAGTAC 1020  
QY 341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu 360  
DB 1021 CATACGCTTTTGGCTCAGTGTCAATTCCTTTGTTAATCCCTTTTGTATCATTTG 1080  
QY 361 CysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValAlaArgGlnSerThr 380  
DB 1081 TGTCACAAAACGTTTCAAGAAAGGCTTTCCTGAAATACCTTCTGTGAGAAAGCAATCCAG 1140  
QY 381 ProProHisAsnArgSerIleSerThr 389  
DB 1141 CCACCACACAAACCGCTCAATATCCACT 1167

RESULT 2  
AADS5126  
ID AADS5126 standard; DNA; 1170 BP.  
XX  
AC AADS5126;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE Human H4 receptor wild-type DNA #2.  
XX  
KW Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;  
KW atopic dermatitis; stroke; myocardial infarction; migraine; allergy;  
KW chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;  
KW rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;  
KW asthma; receptor; gene; de.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..1170  
FT CDS  
FT /\*tag= a  
FT /product= "Human H4 protein"  
FT /note= "CDS does not include stop codon"  
FT /partial  
XX  
PN WO2003020907-A2.  
XX  
PD 13-MAR-2003.

PF 30-AUG-2002; 2002MO-US027891.  
 XX 31-AUG-2001; 2001US-0316762P.  
 PR 13-NOV-2001; 2001US-0332657P.  
 XX (MERI) MERCK & CO INC.  
 PA Gallagher MD, Yates SL;  
 XX WPI; 2003-290166/28.  
 XX P-PSDB; AAE36417.  
 DR Novel splice variants of human H4 histamine receptor, H4b and H4c, useful  
 XX for identifying agonists or antagonists of the receptor which are useful  
 PT for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.  
 XX disclosure; Page 56-58; 31pp; English.  
 XX The invention relates to splice variants of human H4 histamine receptor,  
 CC H4b and H4c. The invention is useful for identifying an agonist, the  
 CC antagonist or inverse agonist of a mammalian histamine receptor. The  
 CC agonist, antagonist or inverse agonist of H4b and H4c is useful for  
 CC treating inflammation, asthma, allergy, atopic dermatitis, stroke,  
 CC myocardial infarction, migraine, chronic obstructive pulmonary disease  
 CC (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel  
 CC disease, or psoriasis. The present sequence is human H4 receptor DNA  
 XX  
 SO Sequence 1170 BP; 292 A; 245 C; 231 G; 402 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.85e-119 Length: 1170  
 Score: 1308.50 Matches: 252  
 Percent Similarity: 77.52% Conservative: 48  
 Best Local Similarity: 65.12% Mismatches: 84  
 Query Match: 64.27% Indels: 3  
 Gaps: 3  
 US-10-626-398-10 (1-389) x AAD55126 (1-1170)  
 QY 5 AasSerThrIleAlaLeuThr---SerIleuValIleSerLeuThrPheLeuMetSerLeu 23  
 Db 13 AATAGCAGCATCATATTTATCTAAGACATCGTGTTCCTTACCTTTTATAGTCTCTTA 72  
 QY 24 LeuAlaIleAlaIleMetLeuGlyAenValValIleLeuAlaPheIleValAaArg 43  
 Db 73 GTAGCTTTCTTAAATCTAAGAAATGCTTGGTCTTTAGCTTTTGGTGAACAA 112  
 QY 44 AasLeuArgHisArgSerAenValPhePheLeuAenValIleAlaAaPhePheVal 63  
 Db 133 AACCTTAGACATGAGAGTACTTATTTTCTTAACTTGCATCTGACTCTTTGTG 192  
 QY 64 GlyAlaIleAlaIlePheLeuValIlePheSerSerLeuThrValTrpThrSerGlyVal 83  
 Db 193 GGTGTGATCTTCTTAAATCTAAGAAATGCTTGGTCTTTAGCTTTTGGTGAAC 252  
 QY 84 GluAlaCysValPheTrpLeuIleThrAspValLeuLeuValSerValIleValAsn 103  
 Db 253 GAAATCTGTATTTTGGCTCACTGACTGACTGATCTGATGATGATGATGATGATGAT 312  
 QY 104 IleValLeuIleSerValAspArgValGlnSerValSerAenValValTrpValArgAla 123  
 Db 313 ATGTCTCTCATGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372  
 QY 124 GlnHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143  
 Db 373 CAACATATGCTGCTTGAAGATGTTACTGATGTGTGCGTGTGGTGGTGGTGGTGGT 432  
 QY 144 MetThrAsnGlyPheMetIleLeuIleSerAspSerTrpGlnAenSerThrGlnCys 163  
 Db 433 TTAGTGAATGGCCAAATGATTTCTAGATTTCTGAGATCTTGAAGATGAGATGAGATG 492  
 QY 164 GluProGlyPheLeuValValTrpValPheAlaLeuProThrSerLeuLeuGluPheLeu 183

Db 493 GAACCTGATTTTTTCGAAATGATACATCTTGCATCATCATCATCTTGAATTCGTG 552  
 QY 184 IleProIleLeuLeuValAlaValPheSerAlaHisIleValTrpSerLeuTrpValArg 203  
 Db 553 ATCCAGTCAATCTTAACTGCTTAAATTCATGAAATATTTATTTGAGCCGTGGAAGCGT 612  
 QY 204 GluIleLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223  
 Db 613 GATCATCTCAATGATGCTCCAAAGCCATCTTGCATGATGCT---GCTCTTCCAAATC 669  
 QY 224 HisGlyHisSerCysArgGlnAaPheProAspSerArgAlaThrLeuProAlaArgValGlu 243  
 Db 670 TGTGACACATCTTCAAGAGTATGATCTTCAAGAGATCTTCTTGTGATGACAGAA 729  
 QY 244 ThrThrAlaSerLeuValSerAspValSerArgValSerSerLeuLeuProSerIle 263  
 Db 730 GTTCTGATCTTTCATTCAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 789  
 QY 264 ArgAlaValAsnSerAenValIleAlaSerValMetGlyPheLeuSerHisSerAsp 283  
 Db 790 AGAACCAAGATGAAATGCAATACAAATTTGCTCCAAATGGGTTCTTCCCAATCAGAT 849  
 QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgValLeuAlaVal 303  
 Db 850 TCTGTAGCTTTCACCAAGGAAACATGTTGAATGCTTGAAGCCAGAGATTAAGCCAA 909  
 QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProValSerLeuThr 323  
 Db 910 TCAGTGCCATTTCTTAAAGGAGTGTGCTGTTGCTGAGGCTCATATCTTCTGTTCA 969  
 QY 324 ValIleSerPhePheProGluArgAenLeuThrIleValSerThrTrpValIleAla 343  
 Db 970 ATGTCTCTTCAATTTATCTTCAAGACAGAGCTTCAATCAATGTTGATTAATGCA 1029  
 QY 344 PheTrpLeuGlnTrpPheAenSerPheValAsnProPheLeuValProLeuValVal 363  
 Db 1030 TTTTGCTTCAGTGTCAATCTCTTGTCAATCTCTTGTATCATGATGTGTCAAG 1089  
 QY 364 ArgPheGlnValAlaPheLeuValIleLeuProValArgArgGlnSerThrPro---Pro 382  
 Db 1090 CGCTTTCAAAGGCTTGTGAAATATTTTGTATTAAGAACCACTTACATGACAA 1149  
 QY 383 HisAsnArgSerIleSerThr 389  
 Db 1150 CACAGTGGTCAATCTTCT 1170  
 RESULT 3  
 AAA46023  
 ID AAA46023 standard; cDNA; 1173 BP.  
 AC AAA46023;  
 XX  
 DT 22-AUG-2000 (first entry)  
 XX  
 DE Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.  
 KW Human; G protein coupled receptor; GPCR; transmembrane receptor;  
 KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;  
 KW 89.  
 OS Homo sapiens.  
 XX  
 PN MO200022131-A2.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 13-OCT-1999; 99WO-US024065.  
 XX  
 PR 13-OCT-1998; 98US-00170496.  
 PR 12-NOV-1998; 98US-0108029P.  
 PR 20-NOV-1998; 98US-0109213P.  
 PR 27-NOV-1998; 98US-0110060P.  
 PR 16-FEB-1999; 99US-0120416P.

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PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123945P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 28-MAY-1999; 99US-0137567P.
PR 29-JUN-1999; 99US-0141448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.
PA (AREN-) ARENA PHARM INC.
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT,
PI Gore M, Ilaw CW, Iain I, Lowitz K, White C;
XX WPI: 2000-117986/27.
DR P-PSDB; AAB02831.
XX Non-endogenous, human G protein-coupled receptors for screening receptor,
PT inverse or partial agonists useful as therapeutic agents.
XX Example 1; Page 88-89; 187pp; English.
XX The present invention describes transmembrane receptors, preferably human
CC G protein coupled receptors (GPCR), for which the endogenous ligand is
CC unknown (orphan GPCR receptors). More specifically the present invention
CC relates to non-endogenous, constitutively activated versions of a human
CC GPCR. These non-endogenous human GPCRs can be useful for the direct
CC identification of candidate compounds as receptor agonists, inverse
CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
CC exemplification of the present invention
XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8,88e-119 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 3 Gaps: 3
US-10-626-398-10 (1-389) x AAA46023 (1-1173)
QY 5 AenSerThrlleAlaLeuThr---SerlleYsileSerleuThrpheleuMetSerleu 23
DB 13 AATAGCAACAATCAATTATTCACCTAGCACTCGGTTACTTTAGCATTTTATGTCCTTA 72
QY 24 LeuAlaileAlaileleuMetleuGlyAsnValValleleuAlaPheleleValAspArg 43
DB 73 GTAGCTTTGCTATATGCTAGGAATGCTTTGTCATTTTATGCTTTTGTGGAGCAAA 132
QY 44 AenleuArgHisArgSerAntYrPhePheleuAsnleuAlaileAlaAspPhePheVal 63
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DB 123 AACCTTAGACATCGAAGTAGTATTTTCTTAACTTGCCCATCTGACTCTTTGTG 192
QY 64 GlyAlaileAlaileProleuTyrlleProSerleuThrTyrlleThrseryLyS 83
DB 193 GGTGTGATCTTCATTCCTTTGTTACCTCCCTCACAGCGCTTTCGATGGATTTTGGAAAG 252
QY 84 GlnAlaCyValPheTrpLeuileThrAspTyrlleuCySerThAlaSerValTyrlAsn 103
DB 253 GAAATCTGTATTTTGGCTCACTACTGATCTGTTATGTATGACAGCATCTGTATATTAAC 312
QY 104 lleValleuileSerTyAspArgTyrlGlnSerValSerAsnAlaValTrpTyrlArgAla 123
DB 313 ATGTGCTTCATCAGCTATGATCGATACCTGATGCTTAAAGCTGTGTCTTATGAACT 372
QY 124 GlnHisSerGlyThrTrpTyrlleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 373 CAACTACTGGGGGTTCGAAAGTTTCTCTCGATGCGCGCTTTGGGTGCTGCGCTTC 432
QY 144 MetThrAsnGlyProMetIleleuileSerAspSerTrpGlnAsnSerThrThrglyCys 163
DB 433 TTAGTGAATGGGCCAATGATTTCTAGTTCAAGTCTTGAAGATGAAGTAGTGAATGT 492
QY 164 GluProGlyPheleuLeuTyrlleTyrlPheAlaLeuProThrSerleuGluPheleu 183
DB 493 GAACTGGATTTTTCGAAATGTACATCTTGCCATCACATCATTTCTGGAATTCGTG 552
QY 184 lleProIleleuLeuValAlaTyrlPheSerAlaHisIleTyrlTrpSerleuTyrlAspArg 203
DB 553 ATCCCAAGCATCTTAGTGGCTTATTTTCAACATGAATATTTATGAGCTGTGGAAGCT 612
QY 204 GluTyAsnSerArgCysleuSerHisProValleuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAGAGGTGCAAGCAAGCCATCTGAGTCACTGCT---GTCTTCCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrleuProAlaArglySgu 243
DB 670 TGTGACACTCATTCAGAGTAGTACTATCTTCAAGAGATCTTTCGACATGACAGAA 729
QY 244 ThrThrAlaSerleuGlySerAspLySerArgTyrlleSerSerleuProSerle 263
DB 730 GTTCCTGATCTTCATTCATTCAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 789
QY 264 ArgAlaTyrlAsnSerAsnValleAlaSerlyMetGlyPheleuSerHisSerAsp 283
DB 790 AGAACCAAGATGATGACATATCAATTCCTTCAAAAGGGTTCCTTCCCAATCAGAT 849
QY 284 SerleuAlaLeuGlnGlnArgGlnHisIleGluPheArgAlaArglySerleuAla 303
DB 850 TCTGTAGCTTTCACCAAGGAGACATGTGAATGCTTAGAGCCAGAGATTAGCCAAAG 909
QY 304 SerleuAlaileleuLeuAlaAlaPheAlaileCysTrpAlaProTyrlSerleuThr 323
DB 910 TCACGTGGCATTCCTTTAGGGGTTTTCCTGTCTGTCTGGCTCCCATATTCCTGTTCACA 969
QY 324 ValIleTyrlSerPhePheProGluArgAsnleuThrylsSerThTyrlTyrlHisThrAla 343
DB 970 ATGTGCTTCATTTATTTCCCTCAGCAACAGGTCTTAATCATGTTGGATGAAATGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheleuTyrlProleuCyHisLyS 363
DB 1030 TTTTGGCTTCAGTGGTCAATTCCTTGTTCATCTCTTTGTATCATGTGTGTCACAG 1089
QY 364 ArgPheGlnTyAsAlaPheleuTyrlleleuProValArgArgGlnSerThPro---Pro 382
DB 1090 CGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATAAAAAAGCAACCTCTACATCACACA 1149
QY 389 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTCGCTCAGTATCTTCT 1170
RESULT 4
AAD01124 standard; cDNA, 1173 BP.
ID AAD01124
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XX	AC	AD001124;
XX	DT	02-NOV-2000 (first entry)
XX	DE	Human orphan G protein-coupled receptor hRUP7 cDNA.
XX	KW	Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening; transmembrane receptor; signal cascade; ss.
XX	OS	Homo sapiens.
XX	FT	Key
XX	FT	CDS
XX	FT	Location/Qualifiers
XX	FT	1..1173
XX	FT	/*tag= a
XX	FT	/product= "hRUP7"
XX	FT	/note= "Human orphan G protein-coupled receptor"
XX	PD	WO20001258-A2.
XX	PD	02-JUN-2000.
XX	PF	13-OCT-1999; 99WO-US023687.
XX	PR	20-NOV-1998; 98US-0109213P.
XX	PR	16-FEB-1999; 99US-0120416P.
XX	PR	26-FEB-1999; 99US-0121852P.
XX	PR	12-MAR-1999; 99US-0123946P.
XX	PR	12-MAR-1999; 99US-0123949P.
XX	PR	28-MAY-1999; 99US-0136436P.
XX	PR	28-MAY-1999; 99US-0136437P.
XX	PR	28-MAY-1999; 99US-0136439P.
XX	PR	28-MAY-1999; 99US-0136567P.
XX	PR	28-MAY-1999; 99US-0137127P.
XX	PR	28-MAY-1999; 99US-0137131P.
XX	PR	29-JUN-1999; 99US-0141448P.
XX	PR	29-SEP-1999; 99US-0156555P.
XX	PR	29-SEP-1999; 99US-0156633P.
XX	PR	29-SEP-1999; 99US-0156634P.
XX	PR	29-SEP-1999; 99US-0156653P.
XX	PR	01-OCT-1999; 99US-0157280P.
XX	PR	01-OCT-1999; 99US-0157281P.
XX	PR	01-OCT-1999; 99US-0157282P.
XX	PR	01-OCT-1999; 99US-0157293P.
XX	PR	01-OCT-1999; 99US-0157294P.
XX	PR	12-OCT-1999; 99US-00416760.
XX	PR	12-OCT-1999; 99US-00417044.
XX	PA	(AREN-) ARENA PHARM INC.
XX	PI	Chen R, Dang HT, Liao CW, Lin I;
XX	PI	WPI: 2000-400068/34.
XX	DR	P-PSDB; AA1771297.
XX	PS	Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists.
XX	PS	Claim 25; Page 59; 102pp; English.

CC	healthy and pathological states
XX	
SQ	Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
 Alignment Scores:	
Pred. No.:	8 88e-119
Score:	1308.50
Percent Similarity:	77.52%
Best Local Similarity:	65.12%
Query Match:	64.27%
DB:	3 Gaps: 3
 US-10-626-398-10 (1-389) x ADD01124 (1-1173)	
OY	5 AsnSerThrIleAlaLeuThr---SerIleYsiLseRtleurThrPheLeuMetSerLeu 23
Dd	13 AAATGGCAACATCAATTATTCACTAAGCACTCGTGTACTTTAGCATTTTTATATGCTCTTA 72
OY	24 LeuAlaIleAlaIleMetLeuGlYAsnValVallIleLeuAlaPheIleValAspArg 43
Dd	73 GTAGCTTTTGCTTAATATGCTTAGAAATGCTTTGGTCATTTTAGCTTTTGCTGTCGAATA 132
OY	44 AsnLeuArHisArgSerAsnTrpPhePheLeuAsnLeuAlaIleAlaAspPhePheVal 63
Dd	133 AACCTTAGACATCGAAGTAGATTAATTTTTCTTAACCTTGCGCATTCTCGACTCTTTGTG 192
OY	64 GlYAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrTrippThrserylYls 83
Dd	193 GGGTGATCTCCATTCCTTCTTGTAKATCCCTCACAGCTGTTGCANATGGATTTGGAAAG 252
OY	84 GlHAlaCyvalAPhetripleuileThraspyrileuLeuCystrAlaSerValTyraSn 103
Dd	253 GAATCTGTGATTTTGGCTCACTGACTCTGTTATGATACAGCATCTGATATATAC 312
OY	104 IleValIleuLlserTyrraspArgryrgInserValSerAsnAlaValTrippTyraXgla 122
Dd	313 ATGTGCTCATACGATATATGAAATCGTGTAGCTCAATAGCTGTGCTTATATAGACT 372
OY	124 GlNHISerclYthrTriplysIleAlathrgImetValAlaValTriplIephSerPhe 143
Dd	373 CAACATACACGGGCTTGAAGAATTGTACTCTGAATGGGCCGCTTTGGGTCTGGCCTTC 432
OY	144 MetTrAsnglyProMetIleleuLlserAspSerrTripgInAsnSerThrgluCys 163
Dd	433 TTAGTGAATGGGCAATGATCTTACHTTCAGAGCTTGTGAAGATGAAAGATGATGT 492
OY	164 GluPrGlyPheleuLylsTrpTyrrPhealaleuProthrSerleuLeuGluPheleu 183
Dd	493 GAACCTGGATTTTTTCCGAATGGATACATCTTCCCATCACATATATCTTGGAAATGTGT 552
OY	184 IlleProIleleuLeuValAlaTyrrPheSerAlahisIleTyrrTPSerleuTriplyArg 203
Dd	553 ATCCCACTGATCTTAACTGCTTAATTTCAACATGAATATTTATTTGAGCCTTGGAACGT 612
OY	204 GlulysLeuSerArGyleuSerIhisIleProValleuProSerAspSerSerSerAsp 223
Dd	613 GATCATCTCAGTAGGGGCAAGGCATCTGAGCTGACTGCT--GTCCTTCCAATATC 668
OY	224 HisGlyHisSerCyArGlnAspProAspSerArgalathrLeuProAlaIatglyGlu 243
Dd	670 TGTGACACTCATTCAGAGTAGACTATCTTCAAGAGATCTCTTGTGATCGACGAAA 729
OY	244 ThrThralSerleuGlySerAspIysSerArgValglyvsSerleuLeuProSerIle 263
Dd	730 GTTCTGCAATCTTTTCATTCAAGAGACAAGAGAAAGATAGTCTCATGTTTTCTCA 788
OY	264 ArgAlaTyrrlysAsnSerAsnValIleAlaserIysMetGlyPheLeuSerHisSerAsp 283
Dd	790 AGAACCAAGTGAATAGCAATACATTCCTCCAAAAATGGTCTCTCCCAATCAGAT 849
OY	284 SerLeuAlaleuGlnIargGluHisIleGluLeuPheArgalathrglyslLeuAlalyb 303
Dd	850 TCCTGATCTTTCACCAAGGGAACATGTGAACGTCTTAGACAGAGATTAAGCCAG 909

```
OY 304 SerLeuAlaIleLeuLeuAlaIlePheAlaIleCysTyrPAlaProTyrSerLeuThrThr 323
DB 910 TCACGCGCATCTCTCTAGGGGTTTTCGTGTGGTGGCTCCATATCTCTGTCACA 969
OY 324 ValIleTyrSerPhePheProGluArgAenLeuThrLySerThrTyrPThrIsthrAla 343
DB 970 ATTGTCCTTCATTTATTCCTCAGCAACAGGCTCCATTAATCATTTGGTATGAATGCA 1029
OY 344 PheTyrPLeuGlnTyrPhePheSerPheValaenProPheLeuTyrProLeuGlyHisLy 363
DB 1030 TTTGGCTTCAGTGTCAATTCCTTTGCAATCCCTTTGTATCCATTTGTGCACAAG 1089
OY 364 ArgPheGlnLyAlaPheLeuLySileuProValArgArgGlnSerThrPro---Pro 382
DB 1090 CCCTTCAAAAGCTTCTTGAAAATATTGTATATAAAACCACTCTACATCACA 1149
OY 383 HisaenArgSerIleSerThr 389
DB 1150 CACAGTCGGTCAGTATCTTCT 1170
RESULT 5
ID AAF83203 standard; cDNA; 1173 BP.
XX AAF83203;
AC AAF83203;
DT 09-JUL-2001 (first entry)
DE Human GPCR-like polypeptide, PFI-013 encoding cDNA.
XX G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasphatic;
XX antiinflammatory; vasorelaxant; antidiabetic; anorectic; cytosolic; human;
XX osteopontin; neuroprotective; nociceptive; dermatological; gynecological;
XX signal transduction; 88.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1173
XX FT /tag= a "PFI-013"
XX FT /product= "PFI-013"
XX
XX EPI096009-A1.
XX PD 02-MAY-2001.
XX PF 24-OCT-2000; 2000EP-00309364.
XX PR 29-OCT-1999; 99GB-00025641.
XX PR 20-APR-2000; 2000GB-00009973.
XX PA (PFI2 ) PFIZER LTD.
XX PA (PFI2 ) PFIZER INC.
XX
XX Peter B. O'reilly MA;
XX
XX WPI: 2001-309854/33.
XX DR P-PSDB; AAB62445.
XX
XX New G-protein coupled receptor-like polypeptide, polynucleotide for
XX screening drug candidates for treating diseases associated with signal
XX transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
XX
XX Claim 1; Page 43; 66pp; English.
XX
XX This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor
XX (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be
XX expressed by standard recombinant methodology. Antibodies and modulators
XX of PFI-013 are useful in the manufacture of a medicament for treating
XX allergic disorder, including extrinsic asthma, immunological disorders,
XX such as intrinsic asthma, vasculitic granulomatous disease, interstitial
XX and other pulmonary disease, including chronic obstructive pulmonary
```

```
CC disease (COPD), infectious, inflammatory disease, such as inflammatory
CC bowel disease and neoplastic and myeloproliferative diseases. They are
CC also useful for treating obesity, diabetes, metabolic, neurological
CC diseases, psychotherapeutics, urogenital disease, reproduction and sexual
CC medicine, inflammation, cancer, tissue repair, dermatology, photocuring,
CC skin pigmentation, osteoporosis, cardiovascular, gastrointestinal
CC diseases, allergy and respiratory disease, sensory organ disorders, sleep
CC disorders and hair loss. The PFI-013 protein and nucleic acid are useful
CC in the diagnosis and treatment of the above conditions and also for
CC screening drug candidates for the treatment of diseases associated with
CC signal transduction. The antibodies are also useful for enrichment of
CC eosinophils from mammalian, especially human blood and for detecting the
CC protein in biological samples
XX
SQ Sequence 1173 BP; 294 A; 245 C; 211 G; 403 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8,88e-119 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: Gaps: 3
US-10-626-398-10 (1-389) x AAF83203 (1-1173)
OY 5 AenSerThrIleAlaLeuThr---SerIleLySileSerLeuThrPheLeuMetSerLeu 23
DB 13 MATAGCACAATCAATTTATTCATAGACACTGCTGTACTTTAGCATTTTATATGCTTTA 72
OY 24 LeuAlaIleAlaIleMetLeuGlyAenValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTGGCTAATATCTAGTGAAGAATCTTGTGCTATTTATGCTTTGTGTGACAA 132
OY 44 AenLeuAIGHISArgSerAenTyrPhePheLeuAenLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAGACATCGAAGTATATTTTCTTAATCTGGCCATCTGACCTCTTGTG 192
OY 64 GYAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTyrThrSergLy 83
DB 193 GGTGATCTCTCCATCTCTTTGTACTCTCTACACAGCTGTTGGAATGGATTTTGGAAAG 252
OY 84 GlnAlaCysValPheThrLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAen 103
DB 253 GAATCTGTGATATTTTGGCTCACTACTGACATCTGTTATGACAGCATCTGATATATAC 312
OY 104 IleValIleLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaValTyrArgAla 123
DB 313 ATTGTCTCATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
OY 124 GlnHisSergLyThrTyrPheIleAlaThrGlnMetValAlaValTyrPheSerPhe 143
DB 373 CAACATCTAGGGGCTTGAAGATTTCTACTGATGATGATGATGATGATGATGATGATGAT 432
OY 144 MetThrAenGlyPrometIleLeuIleSerAspSerTyrPheIleAsnSerThrThrGly 163
DB 433 TTAGTGAATGGGCAATGATTTCTAGTCTCAGAGCTTGAAGAGTGAAGTGAATGT 492
OY 164 GluProGlyPheLeuLyLeuTyrPheAlaLeuProThSerLeuLeuIlePheLeu 183
DB 493 GAACCTGGAATTTTTCGAAAGTATGATCTTGCCATCACTCATCTTCTTGAAATTCGG 552
OY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTyrSerLeuTyrPhe 203
DB 553 ATCCAGTCATCTTATGCTTATTTTCAACATGATATTTATGAGCTGTGGAAGCT 612
OY 204 GluLySerSergArgCysLeuSerHisProValLeuProSerAspSerSergSerAsp 223
DB 613 GATCATCTCAGTAGGTGCAAGGATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669
OY 224 HisGlyHisSergCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLySgu 243
DB 670 TGTGACACTCATTCAGAGTATGACTATCTTCAGAGATCTTCTTGTGATCGACAGAA 729
```

QY		244	ThrlrhlalSerleuGLySeAsenSerlySerrgAglvysSerSetleuLeuProSerlle	263
Db		730	GTTCTCGATCCTTTCATTCCAGACAGACAGACGAAAGAAGTAGTCTCATGTTCCTCA	789
QY		264	ArgAlArLyrySaenSerAsenValIleaIserylSwetGlYphleuSerHisSerAp	283
Db		790	AGAACCAGATGAATATAGCAATATACAATTGCTCCAAAATGGGTCTCTCCCAATCAGAT	849
QY		284	SerleuAlaleuLingInIArGlnHslIlegIUleuPheAlAgAlArGlvyleuAlayls	303
Db		850	TCTGTAGCTCTTACCCAAAGGAACVGTGTAAACGCTTAAAGCCAGATTAGCCAAAG	909
QY		304	SerleuAlalieleuleuAlaAlaphelAlileCySTrpAlProTySerleuThrThr	323
Db		910	TCACTGGGCATCTCTTGAGGGGTTTTGCTGTGTCTGAGGCTCCATATCTCTGTCCAC	969
QY		324	VallleTySerphepeProGUarGanleuthrylsSerthrTrPyrrHisThrAla	343
Db		970	ATTGTCCTTCATTTATTCCTCACACACAGGCTCCTTAATCAGTTTGGTATGAAATTGCA	1029
QY		344	PheITrpleuGIntTPPhAsnSerPheAlaIsnPProPheleuTYrProleuCyeHiAlays	363
Db		1030	TTTTGGCTTCAGTGGTTCATAATTCCTTGTGCATCTCTTGTGTATCCATTGTGCACAAG	1089
QY		364	ArgPheGlnlysaAlapheluleylleleuProvalArgArGlnSerThrPro---Pro	382
Db		1090	CGCTTTCAAAAGGCTTCTTTGAAAAATATTTGTATATAAAAAGCAACCTTCACATCACAA	1149
QY		383	HlsaAnaRgsSerieSerThr	389
Db		1150	CACAGTCGGTCAGTATCTTCT	1170
<b>RESULT 6</b>				
AAH24007				
ID	AAH24007	standard; cDNA;	1173 BP.	
XX	AAH24007;			
DT	10-NOV-2001	(first entry)		
DE	Human G protein-coupled receptor AXOR35 cDNA.			
KM	AXOR35; human; G protein-coupled receptor; 7TM receptor;			
KW	histamine H3 receptor homologue; infection; viral; bacterial; fungal;			
KM	proctocoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;			
KM	bulimia; osteoporosis; asthma; allergy; urinary retention;			
KM	acute heart failure; hypotension; hypertension; angina pectoris;			
KM	myocardial infarction; stroke; ulcer; migraine; vomiting;			
KM	psychotic disorder; neurological disorder; depression; anxiety; schizophrenia;			
KM	manic depression; bipolar disorder; depression; delirium; dementia;			
KM	severe mental retardation; dyskinesia; Parkinson's disease;			
KM	Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;			
KM	macrophage; eosinophil; neutrophil; function modulation;			
KM	autoimmune disorder; pulmonary disorder; gene therapy; vaccine;			
KM	drug screening; signal transduction; transgenic animal; drug discovery;			
OS	ss.			
XX				
XX	Homo sapiens.			
Key	Location/Qualifiers			
FT	1..1173			
FT	/tag= a			
FT	/product= "Human AXOR35"			
FT	/note= "G protein-coupled receptor"			
XX				
FN	WO200133221-A1.			
XX				
PD	10-MAY-2001.			
PF	26-OCT-2000; 2000WO-USO29461.			
RR	02-NOV-1999; 99US-00431898.			

PR 03-FEB-2000; 2000US-00497790.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX  
PI Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;  
PI Michalovich D, Morrow DM, Zhu Y;  
XX  
XX WPI; 2001-316464/33.  
DR P-PSDB; AAB73622.  
XX  
XX Novel G-protein coupled receptor polypeptide and polynucleotide for  
PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological  
PT disorders and for identifying modulators useful for treating asthma.  
XX  
PS Claim 2, Page 49-50; 54pp; English.

CC The invention relates to the human G protein-coupled receptor AXOR35  
CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments  
CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative  
CC transmembrane domains and is involved in signal transduction. AXOR35 has  
CC homology and structural similarity with G protein-coupled receptors such  
CC as the human histamine H3 receptor. The invention also relates to  
CC expression vectors and host cells comprising AXOR35 DNA, to recombinant  
CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins  
CC and nucleotides may be used to treat a wide variety of disorders  
CC including bacterial, fungal, protozoal and viral infections, particularly  
CC HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;  
CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;  
CC urinary retention; acute heart failure; hypotension; hypertension; angina  
CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;  
CC psychotic and neurological disorders such as anxiety, schizophrenia,  
CC manic depression, depression, delirium, dementia, and severe mental  
CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's  
CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and  
CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and  
CC antibodies may be used in screening compounds for their ability to  
CC modulate AXOR35 activity or expression. Such AXOR35 modulators are  
CC particularly useful for treating asthma, and inhibiting or promoting the  
CC function of lymphocytes, macrophages, eosinophils or neutrophils in  
CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also  
CC useful for diagnosing or determining susceptibility of an individual to a  
CC disease via the detection of abnormal levels of protein or mRNA, or via  
CC the detection of mutations in the corresponding gene. AXOR35 proteins are  
CC also useful for inducing an immunological response in a mammal against  
CC the above diseases, and for antibody production. AXOR35 nucleotides are  
CC also useful as diagnostic reagents, in chromosome localization and tissue  
CC expression studies, and for producing transgenic animals useful in drug  
CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35  
CC protein or fragments thereof, and are also useful for treating conditions  
CC associated with the expression of the AXOR35 protein. The present  
CC sequence represents cDNA encoding human AXOR35

XX Sequence 1173 BP, 294 A, 245 C, 221 G, 403 T, 0 U, 0 Other;  
XQ

Alignment Scores:	
Pred. No.:	8, 886-119
Score:	1108, 50
Percent Similarity:	77.52%
Best Local Similarity:	65.1%
Query Match:	64.2%
DB:	5
Gaps:	3
length:	1173
Matches:	252
Mismatches:	48
Indels:	84
Gaps:	3

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US-10-626-398-10 (1-389) x AAH24007 (1-1173)

Oy  5  AAmSeThrlIalaleuThr---SerIleYsIleSerIauThrPhleuMetSerIeu 23
    13  AAmGACACATCAATTATCTACTAGCACTCGTGTACTTATGCAATTTTATGTCTTA 72
Db

Oy  24  LeuAlIleAlIleMetIeuGlyAsnValValIleIleuAlaPheIleValaAspArg 43
    73  GmGCTTTTGCTATATATGCTAGAAATCCTTTGTGCATTTTATAGCTTTGTGTGCACAA 122
    :
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QY 44 AenLeuAaHiaArgSerAsnTyrPhePheLeuAenLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAGCATGAGTAGTATATTTTCTTAACCTTGCCATCTCTCTTGTG 192
QY 64 GYAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyAs 83
DB 139 GGTGATCTCCATTCCTTGTGATCCCTCACACGCTTGGAAAGGATTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
DB 253 GAAATCTGTATATTTGGCTCACTACTGACTATCTGTATGACAGCATCTGATATAC 312
QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
DB 313 ATGGCCCTCATCAGCATATGATGATCCCTGACAGTCTCAAAAGCTGTGCTTATGAAC 372
QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 373 CAACATCTGGGCTCTTGAGAGATTGTTACTCTGATGAGGCGGTTGGGCTGGGCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGlyCys 163
DB 433 TAGAGGAATGGGCAATGATTTCTGATGAGTCTTGAGAGATGAAGTAGTAGATGT 492
QY 164 GluProGlyPheLeuLeuLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
DB 493 GAACCTGGATTTTTCGAGATGATGATCCTTGCCATCACAATTCCTTGGAATTCGTG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysAsp 203
DB 553 ATCCAGATATCTTACTGCTTATTTCAACATGAAATTTATGAGCTGTGGAAAGCT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValIleuProSerSerSerSerAsp 223
DB 613 GATCATCTCAGTAGAGGCAAGGCAATCTCTGAGCATGACGT---GTCCTTCCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
DB 670 TGTGACACTCATTCACAGTAGACATATCTCAAGGAGATCTCTTCTTCATCGACAGAA 729
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
DB 730 GTTCTGCGATCTTTCATTCACAGACACAGAGAAAGTAGTCTCATGTTTCTCTCA 789
QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGAATAGCAATACATATGCTTCCAATGGTCTCTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnArgGlnHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB 850 TCTGTAGCTCTTCACCAAGGAACTGTGAACTGCTTAGAGCCAGGAGATTACCAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaIlePheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
DB 910 TCACTGGCCATCTCTTACGGGTTTGTGCTGTGCTGCTCCATATCTCTGTTCA 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrPyrHisThrAla 343
DB 970 ATTGCCCTTCAATTTATTCCTCAGCAACAGGCTCAATATCAGTTGGATGAATTGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
DB 1030 TTTTGCTTCAGTGGTCAATTCCTTGTCAATCCCTTTTATCCATTTGTGTCAAG 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgLysSerThrPro---Pro 382
DB 1090 CCGTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCACTTACATCACA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTGGTCAGTATCTTCT 1170

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, RESULT 7

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ABZ80663
ID ABZ80663 standard; cDNA; 1173 BP.
XX
AC ABZ80663;
XX
DT 13-JUN-2003 (first entry)
XX
DE Human histamine receptor coding sequence.
XX
KW human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;
KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
KW anti-migraine; cardiac; anti-rheumatic; anti-arthritic; antipsoriatic;
KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;
KW myocardial infarction; migraine; chronic obstructive pulmonary disease;
KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
KW psoriasis; receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1173
FT /tag=a
FT /product="Histamine receptor"
FT
XX
EN US6204017-B1.
XX
PD 20-MAR-2001.
XX
PF 07-OCT-1999; 99US-00414010.
XX
PR 07-OCT-1999; 99US-00414010.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Behan JX, Hedrick JA, Laz TM, Monema FJ, Morse KL, Umland SP;
PI Wang S;
XX
DR WPI; 2002-442063/47.
XX
P-PSDB; ABO98629.
XX
PT New nucleic acid encoding antigenic part of human histamine receptor,
PT useful for preparing antibodies, e.g. for treating-histamine related
PT disorders.
XX
PS Example 1; Col 27-28; 19pp; English.
XX
SC This sequence represents the open reading frame for a human histamine
SC receptor (HR) designated SP9144. The sequence was isolated by searching
SC databases with the sequence of known G-coupled protein receptor (GPCR).
SC The gene is used for recombinant production of HR and for preparing
SC antibodies (Ab). These Ab are used to purify HR by immunofinity
SC chromatography, in immunosay of histamine receptor, to identify cDNA
SC clones that express the receptor, as antagonist to block binding of
SC histamine (for treating any histamine-associated disorder) and to
SC generate anti-idiotypic antibodies. Agonists and antagonists of the HR
SC protein can be used in the treatment of e.g. inflammation, asthma,
SC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,
SC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
SC sclerosis, inflammatory bowel disease and psoriasis
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 8,88e-119 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 6 Gaps: 3
US-10-626-398-10 (1-389) x ABZ80663 (1-1173)

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QY 5 AsnSerThrIleAlaLeuThr--SerIleLysIleSerLeuThrPheLeuMetSerLeu 23

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Db      13  AATAGCACAATCATTTATCATCTAGACATCGTGTACTTATGACATTTTATATGCTCTTA 72
Qy      24  LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db      73  GTAGCTTTTCTTAAAGTGGAAAGTGGTGTCTTTAGCTTTTGTGGTGACAAA 132
Qy      44  AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaPhePheVal 63
Db      133  AACCTTAGACATCGAAGTACTTATTTTCTTACTTGGCCATCTGACTTCTTTGTG 192
Qy      64  GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSergly 83
Db      193  GGTGTGATCTCCATCTCTTGTACATCCCTCAACGCTGTGCAATGGATTTTGGAAAG 252
Qy      84  GluAlaGlyValPheTrpLeuIleThrAspTyrLeuLeuGlySerThrAlaSerValTyrAsn 103
Db      253  GAAATCTGTATATTTTGGCTCACTACGACTATCTGTATGTACAGCATCTGTATATAC 312
Qy      104  IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTyrArgAla 123
Db      313  ATTGTCTCTACACTGTATGATCTGACTCTCAATGCTGTCTTATAGAACT 372
Qy      124  GluHisSerglyThrTrpIleAlaIleThrGlnMetValAlaValTrpIlePheSerphe 143
Db      373  CACATCTAGTGGGCTTGAAGATGTACTGTATGTTGGGCCGCTTGGTGGCTGCTTC 432
Qy      144  MetThrAsnGlyProMetIleLeuIleSerAspSerpTrpGlnAsnSerThrTrpGluCys 163
Db      433  TTTAGTAAATGGCCAAATGATTTCAATTTCAGAGCTTGGAAAGGTAGTAAATGT 492
Qy      164  GluProGlyPheLeuIleValTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db      493  GAACCTGGATTTTTCGAAATGTACATCTTCCCATCATCATCTTGGAAATTCGTG 552
Qy      184  IleProIleLeuLeuValAlaIleTyrPheSerAlaHisIleTyrTrpSerLeuTyrArg 203
Db      553  ATCCAGTCACTTACGCTTATTTCAACATGAAATTTATGAGACCTGTGGAACGT 612
Qy      204  GluIleLeuSerArgCysLeuSerHisProValLeuProSerAspSerpSerSerAsp 223
Db      613  GATCATCTCAGTAGTGCCTCAAGGCATCTGAGTGTACTCT--GTCTCTTCCAAATC 669
Qy      224  HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgGlyGlu 243
Db      670  TGTGACACTCATTCACAGGTAGACTATCTTCAAGGATCTCTTGTGATGCACAGAA 729
Qy      244  ThrThrAlaSerLeuGlySerAspIleSerArgIleGlySerSerLeuLeuProSerphe 263
Db      730  GTTCTGCAATCTTTTCAATTCAGAGACAGAGAGAAAGTAGTCTCATGTTTCTCA 789
Qy      264  ArgAlaTyrIleAsnSerAsnValIleAlaSerIleMetGlyPheLeuSerHisSerAsp 283
Db      790  AGAACCAAGATGAAATACCAATGCTTCCAAATGGGTTCTCTTCCCAATCAGAT 849
Qy      284  SerLeuAlaLeuGlnGlnIleArgGlyHisIleGlyLeuPheArgAlaArgIleAlaVal 303
Db      850  TCTGACTCTTTCACCAAGGAAAGATGTGAAGCTTGAAGCAGAGAAATTAAGCCAG 909
Qy      304  SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
Db      910  TCATGCGCATCTCTTAAGGGTTTGTGCTGTGCTGGGCTCATATTCCTGTTACA 969
Qy      324  ValIleTyrSerPhePheProGluArgAsnLeuThrIleSerpheThrTyrTrpIleHisThrAla 343
Db      970  ATTGTCTTCTTATTTTCTTCCAGCAACAGTCTTAAATCAGTTTGTATAGAAATTTGCA 1029
Qy      344  PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrTrpLeuCysHisIle 363
Db      1030  TTTTGGCTTCAAGTGTCAATCTTGTGTCAATCTTGTGTATCCATGTGTGACAG 1089
Qy      364  ArgPheGlnIleValAlaPheLeuIleLeuProValAlaArgIleSerpheThrPro--Pro 382

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Db      1090  CGCTTCAAAAGCGTTCTTCAAAAATATTTGTATATAAAAGCACTTACATCACAA 1149
Qy      383  HisAsnArgSerIleSerThr 389
Db      1150  CACAGTGGTCAATCTTCT 1170

RESULT 8
ABQ78739
ID  ABQ78739 standard; DNA; 1173 BP.
AC  ABQ78739;
DT  05-DEC-2002 (first entry)
XX
DE  Nucleotide sequence of human histamine receptor.
XX
KW  Human; histamine receptor; receptor; inflammation; asthma; allergy;
KW  atopic dermatitis; stroke; myocardial infection; migraine;
KW  chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;
KW  multiple sclerosis; inflammatory bowel disease; psoriasis;
KW  intracellular second messenger pathway; cellular growth rate;
KW  hormone secretion; gene; 88.
XX
OS  Homo sapiens.
XX
FH  Key 1.1173
FT  CDS /tag=a
FT  /product="histamine receptor"
XX
PN  US2002098539-A1.
XX
PD  25-JUL-2002.
XX
PF  19-MAR-2001; 2001US-00812216.
XX
PR  07-OCT-1999; 99US-00414010.
XX
PA  (BEHA/) BEHAN J X.
PA  (HEDR/) HEDRICK J A.
PA  (LAZT/) LAZ T M.
PA  (MONS/) MONSMA F J.
PA  (MORS/) MORSE K L.
PA  (UMLA/) UMLAND S P.
PA  (WANG/) WANG S.
XX
PI  Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP,
PI  Wang S;
PI  WPI: 2002-673827/72.
DR  P-PSDB; ABB78276.
XX
PT  Novel mammalian histamine receptor polypeptide useful for identifying
PT  agonist or antagonist for treating diseases such as inflammation, asthma,
PT  stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
XX
PS  Example 1; Page 15-16; 21pp; English.
XX
CC  The present sequence encodes a human histamine receptor. The polypeptide
CC  is useful for identifying an agonist or antagonist of a mammalian
CC  histamine receptor. It is useful as an antigen to elicit the production
CC  of antibodies. The histamine receptor polypeptide and polynucleotide are
CC  useful in the treatment and management of diseases such as inflammation,
CC  asthma, allergy, atopic dermatitis, stroke, myocardial infection,
CC  migraine, chronic obstructive pulmonary disease (COPD), rheumatoid
CC  arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.
CC  They are also useful for modulating intracellular second messenger
CC  pathway activated through histamine receptors (cyclic-AMP, calcium,
CC  inositol phosphate and mitogen activated protein (MAP) kinase), changes
CC  in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+
CC  mobilization, mitogenic effects, etc
XX
SQ  Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

```

## Alignment Scores:

Pred. No.:	8,88e-119	Length:	1173
Score:	1308.50	Matches:	252
Percent Similarity:	77.52%	Conservative:	48
Best Local Similarity:	65.12%	Mismatches:	84
Query Match:	64.27%	Indels:	3
	6	Gaps:	3

US-10-626-398-10 (1-389) x ABQ8739 (1-1173)

```

QY 5 AmsSerThrlleAlaLeuThr---SerlleYsileSerleuThrPheleuNetSerleu 23
DB 13 AATACACACATCAATTTATACCTAGACACTCGTTTACTTGTAGCAATTTTATGCTTTA 72
QY 24 LeuAlaileAlaileMerleuGlyAenValValleleuAlaPheleValAsparG 43
DB 73 GTAGCTTTGCTTAAATGCTAGGAAATGCTTTGCTATTGCTTTTGTGGTGAACAA 132
QY 44 AenLeuAriGhiAArgSerAenTYrPhePheleuAenLeuAlaileAlaAspPheVal 63
DB 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCCATCTGTGACTTCTTGG 192
QY 64 GlyAlaileAlaileProleuTYrleProSerSerleuThrTYrTrpTrpSerGlylys 83
DB 193 GGTGTGATCTCCATTCCTTTGACATCCCTCACAGCTGTTCGAATGGGATTTGGAAAG 252
QY 84 GlnAlaCyValPheTrpLeuileThrApyTYrLeuLeuCySerThAlaSerValTYrAen 103
DB 253 GAAATCTGTATTTTGGCTCACTAGCTATCTGTATGTACAGACTGTATATAC 312
QY 104 lleValleleuileSerTYrAenAryTYrGlnSerValSerAenAlaValTrpTYrAga 123
DB 313 ATGTCTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
QY 124 GlnHissSerGlyThrTrpYsileAlaThrGlnMerValAlaValTrpIlePheSerPhe 143
DB 373 CAACACTACTGGGGCTTGAAGATGTTACTCTGATGCTGGCGTGGTGGCTGCTTC 432
QY 144 MetThrAenGlyProMetIleleuileSerAenPserTrpGlnAenSerThrThrgluCys 163
DB 433 TTAGGGAATGGGCAATGATTTCTAGTTTCAAGCTCTGGAAGATGAGTGAATGAT 492
QY 164 GluProGlyPheleuYsileTYrTYrPheAlaLeuProThrSerleuGluPheleu 183
DB 493 GAACCTGGATTTTTCGGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 552
QY 184 lleProIleleuLeuValAlaTYrPheSerAlaHissileTYrTrpSerleuTrpYsArg 203
DB 553 ATCCCAAGTATCTTAGTCCCTTATTTCAACATGAATATTATTTGAGCTGTGGAAGCT 612
QY 204 GluYsLeuSerAryCySerleuSerHisProValLeuProSerAenPserSerSerAap 223
DB 613 GATCATCTCAAGTAGGTCGAAGGCAATCTTGACATGACGCT---CTCTCTTCCAACATC 669
QY 224 HisGlyHissSerCyAryGlnAenProAenPserAryGalaThrleuProAlaAryGlu 243
DB 670 TGTGACACTCATTTAGAGTAGTACATATTCAAGAGATCTCTTCTTCATCGACAGA 729
QY 244 ThrThrAlaSerleuGlySerApySerAryAryGlySerSerleuLeuProSerle 263
DB 730 GTTCTGCACTCTTTCATTCAGAGACACAGAGAGAAAGTAGTCTTCCTTCCTCA 789
QY 264 ArgaAlaTYrLyAenSerAenValileAlaSerlySmeGlyPheleuSerHisSerAap 283
DB 790 AGAACCAAGATGAATAGCAATACATNTGCTTCCAAATGGTCTCTTCCCAATCAGAT 849
QY 284 SerleuAlaLeuGlnAryGlnHisileGluLeuPheAryAlaAryGlyLeuAlaYs 303
DB 850 TCTGTAGCTCTTACCAAGGGAACATGTTGAATGCTTAGAGCCAGAGATTAAGCAAG 909
QY 304 SerleuAlaileleuLeuAlaPheAlaileCySerThAlaProTYrSerleuThrTrp 323

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DB 910 TCAGTGGCCATCTCTTAGGGGTTTTGCTGTTGGCTGGGCTCCAAATTCCTGTTCACA 969
QY 324 ValileTYrSerPhePheProGlnAryAenLeuThrYsSerThTrpTYrHisThrala 343
DB 970 ATGTGCTTTCAATTTATTTCCACAGCAAGGTCTCTTAATCATGTTGGTATGAAATGCA 1029
QY 344 PheTYrleuGlnTrpPheAenSerPheValAenProPheleuTYrProleuCyHislyls 363
DB 1030 TTTTGGCTTCAAGTGGTCAATCTTTGTCAATCTCTTTTGTATTCATTTGTCACAAAG 1089
QY 364 ArpPheGlnYsAlaPheleuYsileleuProValAryGlnSerThrPro---Pro 382
DB 1090 GCCTTCAAAAGGCTTCTTGAATAATTTGTATTAATAAGCACTCTTACCAACACA 1149
QY 383 HisAenArySerleSerThr 389
DB 1150 CACAGTCCGTAGTATCTTCT 1170

```

## RESULT 9

AA170980  
ID AA170980 standard; cDNA; 1173 BP.

AA170980;

AC 18-MAR-2002 (first entry)

DE Human histamine H4 receptor cDNA.

KW Histamine H4 receptor; human; antihistaminic; antiallergenic;

KW antinflammatory; cardiac; circulatory; antidiabetic; laxative;

KW diagnosis; gene therapy; ss.

OS Homo sapiens.

PN WO200192485-A1.

PD 06-DEC-2001.

PF 22-FEB-2001; 2001WO-US005914.

PR 31-MAY-2000; 2000US-0208260P.

PA (ORTHO-MCNEIL PHARM INC.

PI Lovenberg T, Liu C;

DR WPI: 2002-11439/15.

PS P-PSDB: AAM50564.

PT New mammalian histamine H4 receptor proteins and polynucleotides encoding

PS the proteins, useful in gene therapy for treating diseases where it is

PS beneficial to elevate mammalian histamine H4 receptor activity.

PS Claim 4; Fig 1; 92pp; English.

XX The present sequence is that of cDNA clone pH4R encoding a human  
 CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone  
 CC marrow cDNA library. The invention provides mammalian (human, mouse, rat  
 CC and guinea pig) histamine H4 receptor nucleic acid molecules (see  
 CC AA170980-83) and polypeptides (see AAM50564-67). The nucleic acids have  
 CC been expressed in recombinant host cells that produce active recombinant  
 CC protein. The pharmacology of known histamine ligands is demonstrated.  
 CC Mammalian histamine H4 receptor may be used in gene therapy for the  
 CC treatment of diseases where it is beneficial to elevate mammalian  
 CC histamine H4 receptor activity. Recombinant protein is useful for  
 CC identifying modulators of the human histamine H4 receptor. Such  
 CC modulators may be useful for diagnosing, treating or preventing asthma,  
 CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-  
 CC insulin dependent diabetes mellitus, hyperglycemia, constipation,  
 CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity  
 CC

Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8,88e-119 Length: 1173  
 Score: 1308.50 Matches: 252  
 Percent Similarity: 77.52% Conservative: 48  
 Best Local Similarity: 65.12% Mismatches: 84  
 Query Match: 64.27% Indels: 3  
 DB: 6 Gaps: 3

US-10-626-398-10 (1-389) x AA170980 (1-1173)

QY 5 AAmSerThrIleAlaLeuThr---SerIleValSerLeuThrPheLeuMetSerLeu 23  
 DB 13 AATAGACAAATCAATTTATCATCACTGCTGTTACTTACATTTTATGCTCTTA 72  
 QY 24 LeuAlaIleAlaIleLeuLeuGlyAsnValValIleLeuAlaPheIleValaParg 43  
 DB 73 GTAGCTTTGCTAATAGCTAGGAAATGCTTGCTGATTTTACCTTTGGGGAGCAAA 132  
 QY 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaPhePheVal 63  
 DB 133 AACCTTAGACATGGAAGTACTTTTCTTAACTGGCCATCTCTGACTCTTTG 192  
 QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSergIly 83  
 DB 193 GGTGTGATCTCCATCTCTTGTGATCCCTCACACCTGTTGCAATGGGATTTGGAAAG 252  
 QY 84 GluAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValIlyAsn 103  
 DB 253 GAAATGTGTATTTGGCTGACTGACTGATCTGTATGACACATCTGTATATAC 312  
 QY 104 IleValLeuIleSeryTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123  
 DB 313 ATTGCTCATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372  
 QY 124 GlnHisSerGlyThrTrpIlyValIleAlaThrGlnMetValAlaValTrpIlePheSerphe 143  
 DB 373 CAACATACCTGGGGCTTTGAAAGATTGTACTCTGATGATGGCCGTTGGGCTGGCTTC 432  
 QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163  
 DB 433 TTAGTGAATGGGCAATGATTTAGTTTCAAGATCTTGGAAGATGAAGTACTGATG 492  
 QY 164 GluProGlyPheLeuIlySeryTrpTyrPheAlaLeuProThrSerLeuGlnPheLeu 183  
 DB 493 GAACTGGATTTTTCGGAATGATGATGATGATGATGATGATGATGATGATGATGATG 552  
 QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpIlyAsn 203  
 DB 553 ATCCGAGTACTTATGCTGCTTATTTCAACATGATATTATTATGAGCGCTGGAAAGCGT 612  
 QY 204 GluIlyLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223  
 DB 613 GATCATCTAGTAGGAGCCAAAGCCATCTCGACTGCTCT---GTTCTTCCAAACATC 669  
 QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgIlyGln 243  
 DB 670 TGTGACACTCATCTTCAAGAGTATCTTCAAGAGATCTTCTTGCATGACAGAA 729  
 QY 244 ThrThrAlaSerLeuGlySerAspIlySerArgIlySerSerLeuLeuProSerIle 263  
 DB 730 GTTCTCGATCTTTCATTCAGAGACAGAGAGAAAGTACTGTTCTTCTCA 789  
 QY 264 ArgAlaTyrIlyAsnSerAsnValIleAlaSerIlyMetGlyPheLeuSerHisSerAsp 283  
 DB 790 AGAACCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 849  
 QY 284 SerLeuAlaLeuGlnGlnArgIlyHisIleGlnLeuPheArgIlyArgIlySerLeuAla 303  
 DB 850 TGTGTGCTCTTACCAAGAGGACATGTTGAATGCTTTAGACCCAGAGATTAAGCCAG 909  
 QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323  
 DB 910 TCACCTGGCATCTCTTAAAGGGTTTGGCTGTTGGCTGCTCATATTTCTGTTCAACA 969

QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrIlySerThrTrpTyrHisThrAla 343  
 DB 970 ATGTCTCTTCAATTTATTCCTCAGACAGAGGCTTAAATCACTGTTGATGATGCA 1029  
 QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisIly 363  
 DB 1030 TTTGGCTTCAAGTGTCAATTCCTTGTCAATCCCTTTGTATCATGTTGTCAAG 1089  
 QY 364 ArgPheGlnIlyAlaPheLeuIlyIleLeuProValArgArgGlnSerThrPro---Pro 382  
 DB 1090 CGCTTCAAAAGGCTTCTTGAAATATTTGTATTAAGCAACCTTACATCACA 1149  
 QY 383 HisAsnArgSerIleSerThr 389  
 DB 1150 CACAGTGGTCAATCTTCT 1170

RESULT 10  
 AA167750  
 ID .AA167750 standard; cDNA; 1173 BP.  
 XX  
 AC AA167750;  
 XX  
 DT 27-FEB-2002 (first entry)  
 XX  
 DE Human histamine H4 receptor protein encoding cDNA.  
 XX  
 KW Histamine receptor; H4; antihistaminic; antiasthmatic; immunosuppressive;  
 KW antiallergic; neuroprotective; antidiabetic; human;  
 KW cerebroprotective; cAMP modulator; gene therapy; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..1173  
 FT CDS /tag= a  
 FT /product= "histamine H4 receptor"  
 XX  
 PN MO200185786-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 04-MAY-2001; 2001WO-US014527.  
 XX  
 PR 05-MAY-2000; 2000US-0202151P.  
 PR 23-AUG-2000; 2000US-0227567P.  
 PR 13-NOV-2000; 2000US-0247855P.  
 XX  
 PA (AMHP ) AMERICAN HOME PROD CORP.  
 XX  
 PI Jones PG, Blatcher M, Wu S, Pauech MH;  
 XX  
 DR MPI; 2002-049442/06.  
 DR P-PDB; AAC66023.  
 XX  
 PT New histamine receptor, termed H4 useful for detecting H4 (ant)agonists  
 PT for treating transplanted organ rejection, asthma, allergy, multiple  
 PT sclerosis and rheumatoid arthritis.  
 XX  
 PS Claim 13; Fig 1; 66pp; English.  
 XX  
 CC The invention provides an isolated histamine receptor, H4, which binds  
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4  
 CC receptor can be expressed by standard recombinant methodology. Cells  
 CC expressing H4 receptor protein at a detectable level can suppress cyclic  
 CC adenosine monophosphate (cAMP) formation when contacted with the H4  
 CC receptor agonist. The H4 receptor and antibodies are used for identifying  
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful  
 CC for treating transplanted organ rejection, asthma, allergies and  
 CC autoimmune pathologies such as multiple sclerosis, type I diabetes,  
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor  
 CC protein and nucleic acids are useful targets to identify drugs that are  
 CC effective in treating disorders associated with histamine-regulated

CC processes. Identification and isolation of H4 receptor provides for  
 CC development of screening of molecules that interact with H4 receptors.  
 CC Genetic variants of H4 can be used to diagnose an H4 associated disease  
 CC as described above. The H4 receptor polynucleotide is useful to treat or  
 CC prevent a disorder associated with the function of H4 in peripheral blood  
 CC leukocytes. The present sequence represents a cDNA encoding the human  
 CC histamine H4 receptor protein

XX  
 SQ Sequence 1173 BP; 296 A; 245 C; 231 G; 401 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	8,88e-119	Length:	1173
Score:	1308.50	Matches:	252
Percent Similarity:	77.52%	Conservative:	48
Best Local Similarity:	65.12%	Mismatches:	84
Query Match:	64.27%	Indels:	3
DB:	6	Gaps:	3

US-10-626-398-10 (1-389) x AA167750 (1-1173)

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OY 5 AenserrThrlleAlaLeuthr---SerlleYsileSerleuthrPheleuMetSerleu 23
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 13 AATAGACAAATCAATTTATCTACTAGACACTCGTGTACTTTAGCATTTTATGTCCTTA 72
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 24 LeuAlaileAlaileuLeuGlyAsnValValilleLeuAlaPheilleValAsparG 43
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 73 GTAGCTTTGTATATAGCTAGGAATGCTTGGTCATTTAGCTTTTGTGGTGCAAA 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 44 AenleuAghleAysSerantYrPhePheleuAenleuAlaileAlaAspPheleVal 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 133 AACCTTAGACATGAGTAGATATATTTTCTTAATCTGGCAATCTGACATCTTTGTG 192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 64 GAlaAlaileAlaileProleuYrileProSerSerleuthrYrTrpThrseryGlyS 83
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 193 GGTGATCTCCATCTCTTGTACATCCCTCACAGCCTTGGATGGATTTGGAAAG 252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 84 GlnAlaCyValPheTrpLeuileThraPyrleuLeuCySerThraAlaSerValYrAsn 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 253 GAAATCTGTATTTTGGCTCACTGACTGACTATCTGTATGTAGACATCTGTATATAC 312
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OY 104 lleValleuileSerTrpAsparGTrgInSerValSerAsnAlaValTrpYrArgAla 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 313 ATGTGCTTCATAGCATGATGATGATACCTGATCTCAAAAGCTGTATATGAACT 372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 124 GlnHleSerGlyThrTrpYsileAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 373 CAACATACGGGGCTGTGAAGATTGTACTGTGATGTCGCCCTTGGTGGCTGCCTTC 432
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 144 MetThrAsnGlyProMetIleLeuileSerAspSerTrpGlnAsnSerThrThrgIuCyS 163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 433 TTAGTGAATGGGCAATGATTCAGTTTCAGAGTCTTGGAAAGATGAAGTAGTGAATGT 492
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 164 GluPProGlyPheleuYsTrpYrPheAlaAlaProThrsSerleuLeuGluPheleu 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 493 GAACCTGGATTTTTCGGAATGTGATCATCTGCCATCACAATCTCTTGAATTCGCG 552
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 184 lleProilleLeuValAlaTrpPheSerAlaHleleYrTrpSerleuTrpYsArg 203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 553 ATCCAGATATCTTACTGCTTATTTTCAACATGAATATTTATGAGCCTGTGGAAGCT 612
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 204 GluYsLeuSerArgCySerleuSerHisProValLeuProSerAspSerSerSerAsp 223
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 613 GATCATCTCAGTAGGGCCAAAGCCATCTCGACTCAGTCGCT---GTCTCTTCAACATC 669
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 224 HlSGlyHisSerCyArgGlnAspProAspSerArgAlaThlleuProAlaArgylsGlu 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 670 TGTGACACTCATCTCAGAGTAGACTATCTTCAAGAGATCTCTTCTGCAATCGACAGA 729
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 244 ThrThrAlaSerleuGlySerAspYsSerArgYsSerSerleuProSerile 263
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 730 GTTCTGCAATCTTTTCATTCAGAGAGACAGAGAGAAAGTAGTTCATGTTTCTCTCA 789
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 264 ArgAlaTrpYsAsnSerAsnValilleAlaSerYsMetGlyPheleuSerHisSerAsp 283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 790 AGAACCAAGATGAATAGCAATATCAATTCCTTCAAAATGGGTTCTCTCCCAATCAGAT 849
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 284 SerleuAlaileuGlnAlaArgGlnHleleGluLeuPheArgAlaArgylsleuAlaYs 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 850 TCTGTAGCTCTTCAACCAAGGACATGTGATGATGCTCAGAGCCAGAGATTAAGCAAG 909
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 304 SerleuAlaileuLeuAlaAlaPheAlaileCyStrpAlaProYrSerleuThr 323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 910 TCACGTGGCATTTCTTGGGGTTTGTCTGTCTTCTGGGCTCCATATTCCTGTTCACA 969
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 324 ValilleYrSerPhePheProGluArgAsnleuThrYsSerThrTrpYrHisThrAla 343
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 970 ATTGCTCTTCAATTTATTCCTCAGCAACAGGTCCTCAATCAGTTGTATAGAAATTCGA 1029
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheleuYrProleuCyHisYls 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1030 TTTGGCTTCAGGTTCATATCTCTTTGTCATATCTTTTGTATCCATTTGTGTACAAAG 1089
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 364 ArgPheGlnYsAlaPheleuYsileleuProValArgArgGlnSerThrPro--Pro 382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1090 CGCTTCAAAAGGCTTCTGTGAATATTTGTATATAAAACCAACCTCTACATCAGCA 1149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 389 HisAsnArgSerileSerThr 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1150 CACAGTCGTCAGTATCTTCT 1170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
ACAA93262 standard; cDNA, 1173 BP.
ID ACAA93262
AC ACAA93262;
DE 16-JUL-2003 (first entry)
XX
XX
XX Human cDNA encoding GPCR hRUP7.
DE
XX
XX Human; ss; gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;
KW hARE-5; hRUP3; hRUP5; hRUP6; hRUP7; hGPCR27; hARE-1; hARE-2; hRUP1; hG2A;
KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUP4; signalling cascade.
XX
XX Homo sapiens.
XX
XX US2003017528-A1.
XX
XX 23-JAN-2003.
XX
XX 06-JUN-2001; 2001US-00875076.
XX
XX 20-NOV-1998; 98US-0109213P.
XX 16-FEB-1999; 99US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 12-MAR-1999; 99US-0123946P.
XX 12-MAR-1999; 99US-0123946P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136567P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 29-JUN-1999; 99US-014148P.
XX 28-SEP-1999; 99US-0156333P.
XX 29-SEP-1999; 99US-0156555P.
XX 29-SEP-1999; 99US-0156634P.
XX 12-OCT-1999; 99US-00417044.
XX
XX (CHEN/) CHEN R.
XX (DANG/) DANG H T.
XX (LIAM/) LIAM C W.
XX (LINI/) LIN I.
XX
XX Chen R, Dang HT, Liam CW, Lin I;

```

DR WPI: 2003-428952/40.  
 DR P-PSDB; ABU92265.  
 XX  
 PT Novel endogenous, orphan, human G protein-coupled receptors useful for  
 PT identification of modulators of the receptor and as research tools for  
 PT understanding the role of the receptor in human body.  
 XX  
 PS Claim 25; Page 22; 54pp; English.  
 XX  
 CC The invention relates to a human G protein-coupled receptor (GPCR)  
 CC appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named  
 CC hARE-3, hARE-4, hARE-5, hRUP3, hRUP6, hGPCR27, hARE-1, hARE  
 CC -2, hRP1, hG2L, hCHN3, hCHN4, hCHN5, hCHN6, hCHN7, hCHN8, hCHN9, hCHN10 and hUPF4.  
 CC Also included are a plasmid comprising a vector and one of the cDNAs  
 CC above and a host cell comprising the plasmid. The GPCRs are useful for  
 CC the direct identification of candidate compounds as inverse agonists,  
 CC agonists or partial agonists. In vitro and in vivo systems incorporating  
 CC GPCRs is useful for elucidating and understanding the roles these  
 CC receptors play in the human condition, both normal and diseased, as well  
 CC as understanding the role of constitutive activation as it applies to  
 CC understanding the signalling cascade. The cDNAs are useful for making a  
 CC probe for dot-blot analysis against tissue mRNA and/or RT-PCR  
 CC identification of the expression of the receptor in tissue samples. The  
 CC present sequence is a cDNA encoding a GPCR of the invention  
 CC  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8, 88e-119 Length: 1173  
 Score: 1308.50 Matches: 252  
 Percent Similarity: 77.52% Conservative: 48  
 Best Local Similarity: 65.12% Mismatches: 84  
 Query Match: 64,27% Indels: 3  
 DB: 8 Gaps: 3  
 US-10-626-398-10 (1-389) x ACA93262 (1-1173)  
 QY 5 AanserThllelealeuThr---SerlleylelleSerleuThrPheleuMetSerleu 23  
 DB 13 NATGACACATCAATTATTCATAGACACTCGTGTACTTACATTTTATGATCTCTTA 72  
 QY 24 LeuAlaileAlaileMetleuGlyAenValIvalIleleuAlaPheIleValaPars 43  
 DB 73 GTAGCTTTGCTATATGCTAGGAATGCTTGCTATTTAGCTTTTGCGTGACAA 132  
 QY 44 AenleuArgHieArgSerAntYrPhePheleuAenleuAlaileAlaPhePheVal 63  
 DB 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGCCATCTGCTCTTGTG 192  
 QY 64 GlyAlaileAlaileProleuYrIleProSerSerleuThrYrTrpHsrGlyys 83  
 DB 193 GGTGATCTCTCCATCTTTGTACATCCCTCACACCTGTCGAATGGGATTTTGAAG 252  
 QY 84 GlnAlaCyValPheTrpPheleuIleThrAspYrLeuLeuCySerHraIaSerValYrAan 103  
 DB 253 GAAATCTGTATTTGGCTCACTACTGACTATCTGTATGTACACATCTGTATTAAC 312  
 QY 104 IlevallleuIleSerYrAspArgYrGlnSerValSerAanIaValIryrYrAgaIa 123  
 DB 313 ATGTCTCATCATGATGATGATACCTGTCACTGCTCAATGCTGTGTATAGAACT 372  
 QY 124 GlnHleSerGlyThrTrpPheIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143  
 DB 373 CAACATACGTGGGTCTTGAAGATGTGTACTGTGATGGCCCTTTGGGGCTGGGCTTC 432  
 QY 144 MetThrAsnGlyPrometIleleuIleSerAspSerTrpGlnAenSerThrHrGlyCys 163  
 DB 433 TTAGTGAATGGGCATATGATCTAGTTTCAAGATCTTTGGAAGATGAAGTGTGATGT 492  
 QY 164 GluProGlyPheleuYsYrTrpYrPheAlaIleuProTherSerleuGluPheleu 183  
 DB 493 GAACCTGATTTTTCGGAATGTGTACATCTTGCCATCATCATCTTGGAAATTCGTG 552

QY 184 IleProIleleuIleValIaIleYrPheSerAlaHleIleYrTrpSerleuTrpYsArg 203  
 DB 553 ATCCAGATCATCTTATCCCTTATTTTCAACATGAAATTTATTTGAGCTGTGGAAGCGT 612  
 QY 204 GluYsleuSerArgCysleuSerHisProvalleuProSerAspSerSerAap 223  
 DB 613 GATCATCTCAGTAGGCGCAAGAACCATCTCGACTGACTGCT---GTCTCTTCAACATC 669  
 QY 224 HleGlyHieSerCyAenGlnAspProAspSerArgAlaThrleuProIlaArglySglu 243  
 DB 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTTCTGCATCGACAGAA 729  
 QY 244 ThrThraIleSerleuGlySerAspYsArgYsSerSerleuProSerIle 263  
 DB 730 GTTCCGCACTCTTTATTCACAGACACAGAGGAAGAAAGTGTCTCATGTTTCTCA 789  
 QY 264 ArgAlaIryrIysAsnSerAanValIleAlaSerIysMetGlyPheleuSerHisSerAap 283  
 DB 790 AGAACCAAGATGAATGCAATCAATTCCTCAAAATGGGCTCTTCCCAATCAGAT 849  
 QY 284 SerleuAlaIleuGlnIleArgGlnHleIleGlyleuPheArgAlaArglyIleuAlaYs 303  
 DB 850 TCTGTAGCTCTTCCACCAAGGAAACATGTGAATCTTAGAGCCAGAGATTAGCCAAAG 909  
 QY 304 SerleuAlaileleuIleuAlaIlePheAlaileCystrAlaProtyrSerleuThr 323  
 DB 910 TCACGTGCCATCTCTTGAAGGCTTTGCTGTGCTGTGCGCTCCATTTCTGTTCA 969  
 QY 324 ValIleYrSerPhePheProGluArgAenleuThrIysSerThrTrpYrHsrAla 343  
 DB 970 ATGTCTTCAATTTATTCCTCAGACACAGGCTCAATCAATGTTGATAGAAATGCA 1029  
 QY 344 PheTrpPheGlnTrpPheAsnSerPheValaenProPheleuYrProleuCyHsrIys 363  
 DB 1030 TTTTGCTTCAGGTCAATTCCTTGTCAATCTTTGTATTCATTTGTGTACAAAG 1089  
 QY 364 ArgPheGlnIysAlaPheleuYsIleuProvalArgArgGlnSerThrPro---Pro 382  
 DB 1090 CGCTTCAAAAGGCTTCTTGAAGAAATTTGTATTAAGAACCTCTACATCAGAA 1149  
 QY 383 HleAsnArgSerIleSerThr 389  
 DB 1150 CACAGTCGTCAATATCTTCT 1170  
 RESULT 12  
 ADG98759  
 ID ADG98759 standard; cDNA; 1173 BP.  
 AC ADG98759;  
 XX 11-MAR-2004 (first entry)  
 DT Human orphan GPCR cDNA, RUP7.  
 DE Human orphan GPCR cDNA, RUP7.  
 XX Human; G protein-coupled receptor; GPCR; research tool; gene; ss.  
 KW Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH 1.1173  
 FT CDS /tag= a  
 FT /product= "human GPCR protein"  
 PN US2003148450-A1.  
 XX  
 PD 07-AUG-2003.  
 PF 17-OCT-2002; 2002US-00272983.  
 XX  
 PR 20-NOV-1998; 98US-0109213P.  
 PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123946P.

PR 12-MAR-1999; 99US-0123949P.  
PR 28-MAY-1999; 99US-0136436P.  
PR 28-MAY-1999; 99US-0136437P.  
PR 28-MAY-1999; 99US-0136439P.  
PR 28-MAY-1999; 99US-0136439P.  
PR 28-MAY-1999; 99US-0137127P.  
PR 28-MAY-1999; 99US-0137131P.  
PR 28-MAY-1999; 99US-0141448P.  
PR 28-SEP-1999; 99US-0156533P.  
PR 28-SEP-1999; 99US-0156555P.  
PR 29-SEP-1999; 99US-0156634P.  
PR 12-OCT-1999; 99US-00417044.  
XX  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAM/) LIAM C W.  
PA (LINI/) LIN I.  
XX  
XX Chen R, Dang HT, Liam CW, Lin I;  
XX  
XX WPI: 2003-897571/82.  
DR P-PSDB; ADG98760.  
XX  
XX New cDNA encoding a human G protein coupled receptor, useful for making a  
XX probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR  
XX identification of the expression of the receptor in tissue samples.  
XX  
XX Claim 25; SEQ ID NO 13; 52bp; English.

CC The present invention provides novel human G protein-coupled receptor  
CC (GPCR) proteins and their encoding nucleic acids. The invention is useful  
CC for making a probe for dot-blot analysis and for RT-PCR identification of  
CC the expression of the receptor in tissue samples. The invention is also  
CC useful for identifying candidate compounds as inverse agonists, agonists  
CC or partial agonists and as research tools in determining the location of  
CC the receptors within the body. The present sequence is human orphan G  
CC protein-coupled receptor cDNA.

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8,88e-119 Length: 1173  
Score: 1308.50 Matches: 252  
Percent Similarity: 77.52% Conservative: 48  
Best Local Similarity: 65.12% Mismatches: 84  
Query Match: 64.27% Indels: 3  
DB: 10 Gaps: 3

US-10-626-398-10 (1-389) x ADG98759 (1-1173)

QY 5 AaSerThrIleAlaLeuThr---SerIleuYsIleSerLeuThrPheLeuMetSerLeu 23  
DB 13 AATAGCAACAATCAATTATCACTAGCACTCGTGTACTTATGATTTTATATGCTCTTA 72  
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43  
DB 73 GTAGCTTTGCTATATATCTAGGAATGCTTGTGCTATTTGCTTGTGTGACAA 132  
QY 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63  
DB 133 AACCTTAACATCGAAGTAGTATTTTCTTAATCTGGCCATCTGACTCTCTTTG 192  
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyAs 83  
DB 193 GGTGGATCTCCATTCCTTTGTACATCCCTCAGCGTGTTCGATGGATTTGGAAAG 252  
QY 84 GluAlaCysValPheTyrPheIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103  
DB 253 GAATACCTGTGATTTTGGCTCACTACTACTACTGATATGATAGACATCTGATATTAAC 312  
QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTyrArgAla 123  
DB 313 ATGTCTCATACGATATGATGATGATACCTGTCAGTCTCAAAATGCTGTCTTATAGAACT 372

QY 124 GlnHisSerGlyThrTrpIleAlaIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143  
DB 373 CAACACTACGGGCTTTCGAATGATTTCTCTGAGAGGAGGCGTTGGGTGCTGGCCCTTC 432  
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGlyCys 163  
DB 423 TTAGTGAATGGGCCAATGATTTCTAGATCTTGAAGATGAGATAGTGTGAATGT 492  
QY 164 GluProGlyPheLeuValTyrTrpPheAlaLeuProThrSerLeuGlnPheLeu 183  
DB 493 GAACCTGATTTTTCGGAATGGTACATCTTGGCACAATCTTCTGGAATTCGG 552  
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpIleArg 203  
DB 553 ATCCACAGCATCTTATAGTCTGCTTATTTCAACATGAATATTTATGAGCCTGGAAGAGT 612  
QY 204 GluIleLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerAsp 223  
DB 613 GATCATCTCAGTAGGTCGCAAGCCATCTGAGTCTGACTGCTGCT--GTCCTTCCAAATC 669  
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgIleGlu 243  
DB 670 TGTGACACTCATTCAGAGTACAGTACTATCTTCAAGAGATCTTCTGACATCAGACAGA 729  
QY 244 ThrThrAlaSerLeuGlySerAspIleSerArgTyrSerSerLeuLeuProSerIle 263  
DB 730 GTTCTGCTATCTTTCATTCAGAGACAGACAGAGAGAAAGTATGATCTATGTTTCTTCA 789  
QY 264 ArgAlaTyrIleAsnSerAsnValIleAlaSerIleMetGlyPheLeuSerHisSerAsp 283  
DB 790 AGAACCAAGATGAATAGCAATACATTCCTTCCAAAGGGTCTCTCCCAATCAGAT 849  
QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgIleLeuAlaIys 303  
DB 850 TCTGAGCTCTTACCAAGGAGAACATGTGACTGCTTAGAGCCAGGATTAACAG 909  
QY 304 SerLeuAlaIleLeuLeuAlaIleAlaPheAlaIleCysTrpAlaProTyrSerLeuThr 323  
DB 910 TCACGGCCATTCCTTTCAGGGGTTTTCGCTGTTGCTGGGCTCATATCTCTGTTCA 969  
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrIleYsSerThrTrpTyrHisThrAla 343  
DB 970 ATTGCTCTTATTTATCTCTCAGCAACAGTCCCTTAATCATGTTGGATGTGAATGCA 1029  
QY 344 PheTrpLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisIys 363  
DB 1030 TTTTGCTTCAGTGTCAATTCCTTTGTCATCTCTTTGTATCATTTGTGTACAG 1089  
QY 364 ArgPheGlnIleAlaPheLeuIleLeuProValArgArgIleSerThrPro--Pro 382  
DB 1090 CGCTTTCAAAAGGCTTCTTGAATAATTTGTATATAAAAGCAACCTTACATCACA 1149  
QY 383 HisAsnArgSerIleSerThr 389  
DB 1150 CACAGTCGCTCAGTATCTTCT 1170  
RESULT 13  
ID ABS57063 standard; cDNA: 1173 BP.  
ID ABS57063;  
AC ABS57063;  
XX  
XX 28-JAN-2003 (first entry)  
XX  
XX Human cDNA encoding G-protein coupled receptor AXOR35.  
DB Human; ss; gene; G-protein coupled receptor; AXOR35; lymphocyte;  
KW macrophage; eosinophil; neutrophil; infection; transplant rejection;  
KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;  
KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation;  
KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;  
KW psoriasis; urological disease; urinary retention; cardiovascular disease;

XX		myocardial infarction; hypotension; hypertension; pulmonary disorder;
KM		chronic obstructive pulmonary disease; cough; renal disease;
KM		renal ischaemia; arteriosclerosis; athrosisclerosis; psychosis;
KW		neurological disorder; migraine; anorexia; anxiety; schizophrenia;
KM		dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;
XX		graft versus host disease; osteoporosis.
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1173
FT	/tag= A	
FT	/product= "AXOR35"	
XX		
PN	US2002137054-A1.	
PD	26-SEP-2002.	
XX		
PF	20-JUL-2001; 2001US-00910411.	
XX		
PR	02-NOV-1999; 99US-00431898.	
PR	03-FEB-2000; 2000US-00497790.	
XX		
PR	20-OCT-2000; 2000US-00693761.	
PA	(SMIK ) SMITHKLINE BEECHAM CORP.	
PA	(SMIK ) SMITHKLINE BEECHAM PLC.	
XI	Aubard KM, Bergema DJ, Fitzgerald L, Graybill TL, Li X,	
PI	Mihalovitch D, Morrow DM, Zhu Y;	
DR	WPL; 2003-074982/07.	
XX	P-PSTDB; ABG71960.	
PT		
PT	Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infections, gastrointestinal disorders, autoimmune disorders, urological diseases, cardiovascular diseases and cancer.	
PS	Claim 2; Page 21-22; 24pp; English.	
XX		
CC	The invention relates to an isolated G-protein coupled receptor polypeptide, AXOR35 (and its homologues and variants) and its encoding polynucleotide (and its homologue, variants, complements and RNA equivalents). Also included are an anti-AXOR35 antibody, an AXOR35 expression vector, producing a recombinant host cell by introducing the vector into a cell such that the host cell produces AXOR35, a membrane of the host cell expressing AXOR35, identifying/screening for agonists or antagonists of AXOR35 and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue, by administering to the patient AXOR35 agonists or antagonists. The agonist or antagonist identified is useful for treating a disease such as asthma, or for inhibiting or promoting the function of lymphocytes, macrophages, eosinophil, or neutrophils in diseased tissue such as an asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays, for identifying compounds that are agonists or antagonists of AXOR35, as vaccines, or for treating infections (bacterial, fungal, protozoan or viral infections), transplant rejection, gastrointestinal disorders (such as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease), irritable bowel syndrome, vomiting, inflammation (such as atopic dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis, psoriasis), urological diseases (such as urinary retention), cardiovascular diseases (such as myocardial infarction), hypotension, hypertension, pulmonary disorders (such as chronic obstructive pulmonary disease), cough, renal diseases (such as renal ischaemia), arteriosclerosis, athrosclerosis, psychotic and neurological disorders (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such as Parkinson's disease), cancer, obesity, stroke, septic shock, graft versus host disease and osteoporosis. The present sequence is the CDNA encoding AXOR35	
SQ	Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other:	

Score:	1308.50	Matches:	252
Percent Similarity:	77.52%	Conservative:	48
Best Local Similarity:	65.12%	Mismatches:	84
Query Match:	64.27%	Indels:	3
DB:	10	Gaps:	3

US-10-626-398-10 (1-389) x ABS57063 (1-1173)

QY	5	AenSerThrIleAlaLeuThr--SerIleuSilesSerLeuThrPheLeuMetSerLeu	23
DB	13	AATAGCACAATCAATATTATACCTAGACAGCACTCGTACTTATGACATTTTATATGCTCTTA	72
QY	24	LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg	43
DB	73	GTAGCTTTGGCTATATACCTAGGAATGGTTGGTCATTATTAAGCTTTTGTGGGCAAA	132
QY	44	AenLeuAArgHISArgSerAsnTyRphePheLeuAenLeuAlaIleAlaAspPhePheVal	63
DB	133	AACTTACACATCGAAGTAGTATTATTTTCTTAACCTTGCCATCTCTGACTTCTTGAG	192
QY	64	GlyAlaIleAlaIleProLeuTyRlleProSerSerLeuThrTyRTrpHisSerGlyLys	83
DB	193	GCTGGATCTCCATCTCTTTGTAGACATCCCTACACAGCTGTGGAAAGGATTTTGGAAAG	252
QY	84	GlnAlaCysValPheTrpLeuIleThrAspTyRLeuLeuCysThrAlaSerValTyRAsn	103
DB	253	GAAATCTGTATATTTGGCTCACTGCTGACTTCGTATGTATGACACATCTGTATATAC	312
QY	104	IleValleuIleSerTyRAspArgTyRGlinsSerValSerAsnAlaValTrpTyRArgAla	123
DB	313	ATTGCTCCATCAGCTATGATGATGAACTCGTAGTCTCAAAAGCTGTGTCTTATTAAC	372
QY	124	GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe	143
DB	373	CAACACTATGGGGCTTTGAAGATTCTTACTCGATGGTGGCGTTGGGCTGGGCTTC	432
QY	144	MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGluCys	163
DB	433	TTAGGAAATGGGCCAATATCTTCAAGTTTCAGAGCTCTTGAAAGATAGTAGTATGT	492
QY	164	GluProGlyPheLeuLysLysTrpTyRTrpPheAlaLeuProThrSerLeuGluPheLeu	183
DB	493	GAACTGGATTTTTCGGAATGGATCACTCTGCCATCAATCATTTTGGAAATTCGTG	552
QY	184	IleProIleLeuLeuValAlaTyRpheSerAsnHisIleTyRTrpSerLeuTrpLysArg	203
DB	553	ATCCACAGCATCTTAGTGCCTTATTTCAACAAGATATTATTGAGCCTGTGGAAAGCT	612
QY	204	GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp	223
DB	613	GATCATCTCAATAGAGGTGCCAAAGCCATCTGGACGACGCTGCT--GTCCTTCCAAATC	669
QY	224	HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGln	243
DB	670	TGTGGACACTATTCAGAGTAGACTATCTTCAAGAGATCTCTTCTGCATCGACAGAA	729
QY	244	ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle	263
DB	730	GTTCTGTGATCTTTCATTCACAGAGACAGAGAGAAAGTAGTCAATGTTTCTCTCA	789
QY	264	ArgAlaTyRlysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp	283
DB	790	AGAACAAGATGAATAGCAATATTCATTTGCTTCCAAATGGTTCTTCTCCCAATCAGAT	849
QY	284	SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgGlySerLeuAlaLys	303
DB	850	TCTGTAGCTTTCACAAAGGAGAACATGTGAACGCTTAGAGCCAGAGATTAGCCAAAG	909
QY	304	SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyRSerLeuThrTrp	323
DB	910	TCACCTGGCATCTCTTACGGGGTTTTCGTGTTGCTGGGCTCCAAATTCCTGTTCCACA	969
QY	324	ValIleTyRSerPhePheProGlnArgAsnLeuThrLysSerThrTrpTyRHisThrAla	343



```

Db      613 GATCATCTCAGTAGTGCCCAAGCCATCTCGAAGTCTGCT---GTCTCTTCCAAATC 669
Qy      224 HlSGLVHlSerCySarpglnaPProApsSerArgAlathreupProAlaArgylu 243
Db      670 TGGGACATCTTCAAGAGTACATATCTTCAAGAGATCTCTTCTGATGCACAGAA 729
Qy      244 ThrThAlaSerleuGlySerApLySerArgArglySerSerleuLeuProSerile 263
Db      730 GTTCCTGCATCTTTCATTCATCAGAGACAGACAGAGAAAGTGTCTCATGTTTCTCTCA 769
Qy      264 ArgAlaLtyLysAnSerAnVal11eAlaSerLysMetGlyPheLeuSerHlSerAap 263
Db      790 AGAACCAAGATGATGACATATACATATGCTTCCAAATGGTCTCTTCCCATCAGAT 849
Qy      284 SerLeuAlaLeuGlnGlnArgyluHlSllleGluLeuPheArgAlaArgyluSleuAlaLys 303
Db      850 TCTGTACCTTTCACCAAGGGAACATGTTGAACCTGTTAGACCAAGAGATTAGCCAAAG 909
Qy      304 SerLeuAlaLeuLeuAlaAlaPheAlaAlaLeuCySerPAlaProTySerleuThrThr 323
Db      910 TCATGCGCATCTCTCTTAGGGGTTTTCCTGCTTGGCTGGGCTCCATATCTCTGTTCA 969
Qy      324 Val1leTySerPhePheProGluArgAnLeuThrLysSerThrTrpTyHlStrAla 343
Db      970 ATTGCTCTTCAATTTATCTCTCAGCAACAGTCTCTAAATCACTTGGTATGAAATTGCA 1029
Qy      344 PheTrpLeuGlnTrpPheAnSerPheValaAnProPheLeuTyTrProLeuCyHlSlye 363
Db      1030 TTTTGCTTCAGGGTTCATCTCTTGTCAATCTCTTGTATTCATTTGTGTCAAG 1089
Qy      364 ArgPheGlnLysAlaPheLeuLys1leLeuProValaArgArglnSerThrPro---Pro 382
Db      1090 CGCTTCAAAAGCTTCTTGAABATTTTGTATATAAAAGCAACTCATCATCACA 1149
Qy      383 HlSaenArgSerleuSerThr 389
Db      1150 CACAGTCGGTCACTATCTCT 1170

RESULT 15
ID      ADG86374 standard; cDNA, 1173 BP.
XX      ADG86374;
XX      11-MAR-2004 (first entry)
DT      Human endogenous orphan GPCR hrup7 cDNA.
XX      Human; ss; gene; endogenous orphan GPCR; G protein-coupled receptor;
XX      transmembrane domain 6.
OS      Homo sapiens.
XX      US2003229216-A1.
XX      11-DEC-2003.
XX      16-APR-2003; 2003US-00417820.
XX      13-OCT-1998; 98US-00170496.
XX      12-NOV-1998; 98US-0108029P.
XX      20-NOV-1998; 98US-0109213P.
XX      27-NOV-1998; 98US-0110060P.
XX      16-FEB-1999; 99US-0120416P.
XX      26-FEB-1999; 99US-0121852P.
XX      12-MAR-1999; 99US-0123944P.
XX      12-MAR-1999; 99US-0123945P.
XX      12-MAR-1999; 99US-0123946P.
XX      12-MAR-1999; 99US-0123948P.
XX      12-MAR-1999; 99US-0123949P.
XX      12-MAR-1999; 99US-0123951P.
XX      28-MAY-1999; 99US-0136436P.
XX      28-MAY-1999; 99US-0136437P.

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PR      28-MAY-1999; 99US-0136439P.
PR      28-MAY-1999; 99US-0136567P.
PR      28-MAY-1999; 99US-0137127P.
PR      28-MAY-1999; 99US-0137131P.
PR      28-JUN-1999; 99US-0141448P.
PR      27-AUG-1999; 99US-0151114P.
PR      03-SEP-1999; 99US-0152524P.
PR      29-SEP-1999; 99US-0156555P.
PR      29-SEP-1999; 99US-0156633P.
PR      29-SEP-1999; 99US-0156634P.
PR      29-SEP-1999; 99US-0156635P.
PR      01-OCT-1999; 99US-0157280P.
PR      01-OCT-1999; 99US-0157281P.
PR      01-OCT-1999; 99US-0157282P.
PR      01-OCT-1999; 99US-0157293P.
PR      01-OCT-1999; 99US-0157294P.
PR      12-OCT-1999; 99US-00416760.
XX      (CHEN/) CHEN R.
PA      (LIAM/) LIAM C W.
PA      (LOWITZ/) LOWITZ K.
PA      (CHAL/) CHALMERS D T.
PA      (BEHA/) BEHAN D P.
XX      Chen R, Liam CW, Lowitz K, Chalmers DT, Behan DP;
XX      WPI; 2004-052038/05.
XX      P-PSDB; ADG86375.
XX      New cDNA encoding a non-endogenous, constitutively activated version of a
PT      human G protein-coupled receptor, useful for identifying receptor,
PT      inverse or partial agonists having potential applicability as therapeutic
PT      agents.
XX      Example 1; SEQ ID NO 13; 110pp; English.
XX      The invention relates to a cDNA encoding a non-endogenous, constitutively
CC      activated version of a human G protein-coupled receptor comprising hARE-
CC      3 (E133K), hARE-4 (V233K), hARE-5 (A240K), hGPCR14 (I257K), hGPCR27 (G283K),
CC      hARE-1 (E232K), hARE-2 (G285K), hPR1 (L239K), hG2A (K232A), hRUP3 (L224K),
CC      hRUP5 (A236K), hRUP6 (N267K), hRUP7 (A302K), hCHN4 (V236K), hMC4 (V244K),
CC      hCHN3 (S284K), hCHN6 (L352K), hCHN8 (N235K) or h9 (F236K). Also included are
CC      a non-endogenous version of a human G protein-coupled receptor encoded by
CC      the cDNA, a plasmid comprising the vector and the cDNA and a host cell
CC      comprising the plasmid. The cDNA encodes a non-endogenous, constitutively
CC      activated version of a human G protein-coupled A11 receptor comprising
CC      the angiotensin II type 1 receptor hAT1 (F239K), hAT1 (N111A),
CC      hAT1 (ATXK251C3), a domain swap mutant) or hAT1 (A243*). The mutation is of
CC      an amino acid 16 residues from the proline in transmembrane domain 6 and
CC      is usually to a lysine. The cDNA is useful for identifying candidate
CC      compounds as receptor agonists, inverse agonists or partial agonists
CC      having potential applicability as therapeutic agents. The present
CC      sequence is a cDNA (or fragment) for a wild-type human GPCR.
XX      SQ      Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      8,88e-119      Length:      1173
Score:          1308.50      Matches:      252
Percent Similarity: 77.52%      Conservative: 48
Best Local Similarity: 65.12%      Mismatches: 84
Query Match:      64.27%      Indels:      84
DB:              12      Gaps:      3

US-10-626-398-10 (1-389) x ADG86374 (1-1173)
Qy      5 AsnSerThr1leAlaLeuThr---Ser1leLys1leSerleuThrPheLeuMetSerleu 23
Db      13 AAAGCAATCATATTCATCAGAACCACTCGCTACTTACATTTTATATGCTCTTA 72
Qy      24 LeuAla1leAla1leMetleuGlyAnVal1leVal1leLeuAlaPhe1leValaParg 43
Db      73 GTAGCTTTGCTATATGCTAGGAATGCTTGTGCTATTTAGCTTTGTGTGACAA 132

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44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63  
133 AACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGCCATCTGCACCTCTTGCG 192  
64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83  
193 GGTGGATCTCCATTCCTTTGTACATCCCTCACACGCTGTGCAATGGGATTTTGAAAG 252  
84 GlnAlaCysValPheThrLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103  
253 GAAATCTGTGATTTTGGCTACTGACTGATCTGTATGTATGTACAGCATCTGTATTAAC 312  
104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123  
313 ATTGCTCATCAGCATATCGATACCTGTCAGTCTCAATGCTGTCTTATAGAACT 372  
124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143  
373 CAACATACTGGGGCTTGGAAAGATTGTACTGTAGTGTGGCCGTTGGGCTGCGCCTTC 432  
144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGlyCys 163  
433 TTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGCTTGSAGAGATGAAGTAGTAATGT 492  
164 GluProGlyPheLeuLysTrpTyrPheAlaLeuProThrSerLeuGluPheLeu 183  
493 GAACCTGGATTTTTCGGAATGTATCATCCTTGCCATCAGATCATCTTGGAATTCGTG 552  
184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203  
553 ATCCAGATCATCTTGTAGTCCCTTATTTCAACATGAATATTATTATGGAGCCTGTGAAAGCGT 612  
204 GluLysLeuSerAspCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223  
613 GATCATCTCAGTAGGTGCCAAGCAATCCTTGACATGACTGCT--GTCCTTCCACATC 669  
224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243  
670 TGTGACACTCATTCAGAGTAGACTAGACTTCTCAGAGAGATCTCTTCTGCATCGACAGA 729  
244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263  
730 GTTCTCGATCCTTTCATTCAGAGACAGAGAGAGAGATGATCTCATGTTCCTTCA 789  
264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283  
790 AGAACCAAGATGATAGCAATGCAATGCTTCCAAATGGGTTCTTCTCCAAATCAGAT 849  
284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303  
850 TCTGTAGCTCTTACCAAAAGGAACTGTTGAACGCTTAGAGCCAGAGATTAGCCAAG 909  
304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323  
910 TCACCTGGCCATCTCTTAGGGGTTTTGCTGTGGCTGCTCCATATCTCTGTTCACA 969  
324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343  
970 ATTGTCTTTCATTTTATCTTCAGCAACAGGCTCTAAATCAGTTTGGTATAGAAATTGCA 1029  
344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363  
1030 TTTTGGCTTCAGTGGTCAATTCCTTGTCAATCCCTTTGTATCCATTTGTGTACAAAG 1089  
364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro--Pro 382  
1090 CGCTTTCAAAAGGCTTTCGAAAATATTTGTATATAAAAGCAACTCTACCATCACAA 1149  
383 HisAsnArgSerIleSerThr 389  
1150 CACAGTCGGTCAAGTATCTTCT 1170

Search completed: August 5, 2005, 20:42:36  
Job time : 596 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 20:19:26 ; Search time 703 Seconds  
(without alignments)  
3586.948 Million cell updates/sec

Title: US-10-626-398-10  
Perfect score: 2036  
Sequence: 1 MLANNSTALTSIKISLFTL.....LKILPVROSTPPHNSIST 389

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7297361 segs, 3241162794 residues  
Total number of hits satisfying chosen parameters: 14594722

Minimum DB seg length: 0  
Maximum DB seg length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO.epool\_p/US10626398/runat\_02082005\_155808\_2941/app\_query.fasta.1.583  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=trmb -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -OCCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US10626398.OCCN\_1\_1\_723@runat\_02082005\_155808\_2941  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELop=6 -DELext=7

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
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- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
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- 9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
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- 19: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11\_PUBCOMB.seq:\*
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- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2025	99.5	1170	20	US-10-626-445-7
2	2025	99.5	1170	21	US-10-626-126-7
3	2025	99.5	1170	21	US-10-626-398-7
4	1308.5	64.3	1173	9	US-09-812-216-1
5	1308.5	64.3	1173	9	US-09-910-411-1
6	1308.5	64.3	1173	10	US-09-875-076-13
7	1308.5	64.3	1173	10	US-09-875-252-13
8	1308.5	64.3	1173	13	US-10-052-193-1
9	1308.5	64.3	1173	15	US-10-272-983-13
10	1308.5	64.3	1173	15	US-10-354-769-1
11	1308.5	64.3	1173	16	US-10-393-807-13
12	1308.5	64.3	1173	17	US-10-417-820A-13
13	1308.5	64.3	1173	18	US-10-349-253A-1
14	1308.5	64.3	1173	19	US-10-723-955-13
15	1308.5	64.3	1173	19	US-10-782-596-13
16	1308.5	64.3	1173	19	US-10-737-619-1
17	1308.5	64.3	1173	20	US-10-626-445-1
18	1308.5	64.3	1173	21	US-10-616-088-1
19	1308.5	64.3	1173	21	US-10-626-126-1
20	1308.5	64.3	1173	21	US-10-626-398-1
21	1308.5	64.3	1266	10	US-09-891-138A-5
22	1308.5	64.3	1300	10	US-09-852-165-1
23	1308.5	64.3	1300	19	US-10-696-673-1
24	1308.5	64.3	3689	15	US-10-225-567A-628
25	1308.5	64.3	3689	21	US-10-684-206-19
26	1306.5	64.2	1173	15	US-10-290-078-26
27	1306.5	64.2	1265	15	US-10-290-078-25
28	1244	61.1	1176	20	US-10-626-445-5
29	1244	61.1	1176	20	US-10-626-126-5
30	1244	61.1	1176	21	US-10-626-398-5
31	1235.5	60.7	1176	21	US-10-626-126-6
32	1235.5	60.7	1176	21	US-10-626-126-6
33	1235.5	60.7	1176	21	US-10-626-398-6
34	694.5	34.1	1239	21	US-09-891-053-2
35	694.5	34.1	1239	21	US-09-891-053-5
36	694.5	34.1	2700	21	US-10-759-463-5
37	689.5	33.9	1335	9	US-09-350-206-3
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39	689.5	33.9	1335	9	US-09-166-334-3
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41	689.5	33.9	1335	15	US-10-727-021-6
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44	689.5	33.9	2689	9	US-09-350-206-1
45	689.5	33.9	2689	9	US-09-350-206-1

ALIGNMENTS

RESULT 1  
US-10-626-445-7  
; Sequence 7, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; PRIOR FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 7  
 LENGTH: 1170  
 TYPE: DNA  
 ORGANISM: *Cavia porcellus*  
 US-10-626-445-7

## Alignment Scores:

Pred. No.:	3.48e-219	Length:	1170
Score:	2025.00	Matches:	388
Percent Similarity:	99.74%	Conservative:	0
Best Local Similarity:	99.74%	Mismatches:	1
Query Match:	99.46%	Indels:	0
DB:	20	Gaps:	0

US-10-626-398-10 (1-389) x US-10-626-445-7 (1-1170)

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DB      1 ATGTTGGCAAAATACAGTACATCGCTTACATCAATTAATTTCTTTGACATTTTAA 60

QY      21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIle 40
DB      61 ATGCTTTTACTGCTATTCCTATTAATGTAAGCAATGTCGTGCTATTACCTTTTATT 120

QY      41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAsp 60
DB      121 GTGGACAGAAATCTTAGACATCGAAGTATTTACTTTTCTTACCTGGCCATTGCAGAC 180

QY      61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80
DB      181 TTCTTTGGGGTGCAATTGCATTCCTCTGTACATACCTCTCGCTGACTTACCTGAGACT 240

QY      81 SerGlyValGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100
DB      241 TTGGAAACCAAGCTTGTTGTAATTTGGCTTACTGACTATCTTTTATGTAAGCATCT 300

QY      101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrp 120
DB      301 GTGTAAATATATTGTCCTCATCAGCTACGATCCGACATCGTCAATGATCCGATG 360

QY      121 TyrArgAlaGlnHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTrpIle 140
DB      361 TATAGAGCTCAGACACTCTGACCTGGAAATTTGCTACCTACATGATGCTGCTGTGGAA 420

QY      141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160
DB      421 TTCTCTCTTATGACAAATGGCCGATGATTCGATTTTCAGACTCTTTGGCAGATAGCACT 480

QY      161 ThrGluCysGluProGlyPheLeuValTyrTyrPheAlaLeuProThrSerLeuLeu 180
DB      481 ACAGATATGAACTCGATTTTAAAAAGTGTACTTGGCTCCCTCCATCATCTATTATT 540

QY      181 GluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200
DB      541 GAATTCCTGATCCCATCTTGTAGTTGCTTATTTTCAGGCCCATATTTACGAGCCCTG 600

QY      201 TrpLysArgGluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220
DB      601 TGGAAAGCGAAGAACTGACAGGTGCTTCAGCCACCTGTACTCCCTCTGACTCTTTC 660

QY      221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240
DB      661 ACAGATGACACGAGCACTCTGACAGACGACCCGATTCAGAGGCGACTCTGCAGACA 720

QY      241 ArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeu 260
DB      721 CGGAAGAAACAACCTGCTCTCTTGTGTTGACACAGTCAAGAGAAAGCAAGTCTCTTG 780

QY      261 ProSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSer 280
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QY      281 HisSerAspSerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgLys 300
DB      841 CACTCAGATTCCTCGCTCTTTCAGCAAGGAAACATTCGAACTTTTCAGAGCCAGGAAA 900

QY      301 LeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSer 320
DB      901 TTAGCCAAAGCTGCGCCATCTTGTACAGCTTTTGTGCAATTTGTGGCTCCATATCA 960

QY      321 LeuThrTrpValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyr 340
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QY      341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu 360
DB      1021 CATACTGCCCTTTGGCTCAGAGGTTCATTCCTTTGTTAATCCCTTTTGTATCCATTG 1080

QY      361 CysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgLysSerThr 380
DB      1081 TGTACAAACGTTTTCAGAAAGCTTTCCTGAAAATATCTTCTGTGAGAAAGCAATCCAG 1140

QY      381 ProProHisAsnArgSerIleSerThr 389
DB      1141 CCACCACACACCGCTCAATATCCACT 1167

RESULT 2
US-10-626-126-7
; Sequence 7, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
; US-10-626-126-7

Alignment Scores:
Pred. No.: 3.48e-219 Length: 1170
Score: 2025.00 Matches: 388
Percent Similarity: 99.74% Conservative: 0
Best Local Similarity: 99.74% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 21 Gaps: 0

US-10-626-398-10 (1-389) x US-10-626-126-7 (1-1170)

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QY      21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIle 40
DB      61 ATGCTTTTACTGCTATTCCTATTAATGTAAGCAATGTCGTGCTATTACCTTTTATT 120

QY      41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAsp 60
DB      121 GTGGACAGAAATCTTAGACATCGAAGTATTTACTTTTCTTACCTGGCCATTGCAGAC 180

QY      61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80
DB      181 TTCTTTGGGGTGCAATTGCATTCCTCTGTACATACCTCTCGCTGACTTACCTGAGACT 240
  
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QY 81 SerGlyValGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100  
DB 241 TCTGGAAGACGACTGTGTATTTGGCTACTACTACTATCTTTATGTACAGCATCT 300  
QY 101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyr 120  
DB 301 GGTGTAATAATATTTCTCATCACTACACTACGAGCGCTACACGACATCTCAATGCGGTGG 360  
QY 121 TyrArgAlaGlnHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTyrPhe 140  
DB 361 TATAGAGCTCAGACCTGTGGCACTGGAAATTTGCTACTAGATGTGGCTTTGGATA 420  
QY 141 PheSerPheMetThrAnglyPrometIleLeuIleSerAspSerTyrGlnAsnSerThr 160  
DB 421 TTCTCCTTATGACAATGGCCGATGATCTGATTTACAGCTCTTGCGAGATAGACT 480  
QY 161 ThrGluCysGluProGlyPheLeuValbTyrTyrPheAlaLeuProThrSerLeuLeu 180  
DB 481 ACAGAAATGGAACCTGGATTTTAAAGTGGTACTTCTCTCCCTACATCATTAATG 540  
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DB 541 GAATTCCTGATCCCATCTTTGTTAGTTGCTTATTTGACGCCCATATTACTGGAGCTG 600  
QY 201 TrpValArgGluValbLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220  
DB 601 TGGAAAGCAGAGAACTGAGCAGAGCTGTGCTGAGCACTCTGACTCTGACTCTTCC 660  
QY 221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240  
DB 661 AGCAGAGACCCAGACACTCTCTCAGACAGGACCCGATTCAGAGGGGAGACTGCCAGCA 720  
QY 241 ArgValGluThrThrAlaSerLeuGlySerAspLeuSerArgArgIlySerSerLeuLeu 260  
DB 721 CGGAAAGAAACACTGCTCTCTTGGTTCCAGACAGTCCAGAGAAAGACAGACTCTTG 780  
QY 261 ProSerIleAspAlaTyrIlyAsnSerAsnValIleAlaSerIlyMetGlyPheLeuSer 280  
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QY 281 HisSerAspSerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgIly 300  
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QY 301 LeuAlaIlySerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSer 320  
DB 901 TTAGCCAAAGTACCTGGCCATACCTTACAGCTTTGGCCATTTGGCGCTCATATCA 960  
QY 321 LeuThrThrValIleTyrSerPhePheProGluArgAsnLeuThrIlySerThrTyr 340  
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QY 341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu 360  
DB 1021 CATACTGCGCTTTGGCTCCAGCTGTCAATTCCTTTGTATATCCCTTTTGTATCAATG 1080  
QY 361 CysHisIlyAspArgPheGlnIlyAsaIlePheLeuValIleLeuProValArgArgIlySerThr 380  
DB 1081 TGTCAAAAGCTTTTCAAGAGGCTTTCCGAAATACTTCTCTGTGAGAAAGCAATCCAGC 1140  
QY 381 ProProHisAsnArgSerIleSerThr 389  
DB 1141 CCACCAACACACCGCTCAATATCCACT 1167

RESULT 3  
US-10-626-398-7  
; Sequence 7, Application US/10626398  
; Publication No. US20050074841A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlin  
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0034

; CURRENT APPLICATION NUMBER: US/10/626,398  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 1170  
; TYPE: DNA  
; ORGANISM: Cavia porcellus  
; US-10-626-398-7

Alignment Scores:  
Pred. No.: 3,48e-219 Length: 1170  
Score: 2025.00 Matches: 388  
Percent Similarity: 99.74% Conservative: 0  
Best Local Similarity: 99.74% Mismatches: 1  
Query Match: 99.46% Indels: 0  
DB: 21 Gaps: 0

US-10-626-398-10 (1-389) x US-10-626-398-7 (1-1170)

QY 1 MetLeuAlaAsnAsnSerThrIleAlaLeuThrSerIleValIleSerLeuThrPheLeu 20  
DB 1 ATGTTGGCAATATACAGTACCAATCGCCTTACATCAATTAATTTCTTGACATTTTGA 60  
QY 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIle 40  
DB 61 ATCTCTTACTACTCTTGGCTATTAATGTTAGCAATGTCGTGTCAATTTAGCTTTTATT 120  
QY 41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAsp 60  
DB 121 GTGACAGAAATTTAGACTTCGACAGTAATTAATTTCTTACTTGGCATTTGGAGAC 180  
QY 61 PhePheValGlyValIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80  
DB 181 TTTCTTGTGGGTGCATTTGCAATTCCTCTGTACATACCTTCCCTGGTACTTGACT 240  
QY 81 SerGlyValGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100  
DB 241 TCTGGAAGACGACTGTGTATTTGGCTACTACTACTATCTTTATGTACAGCATCT 300  
QY 101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyr 120  
DB 301 GGTGTAATAATATTTCTCATCACTACACTACGAGCGCTACACGACTCAATGCGGTGG 360  
QY 121 TyrArgAlaGlnHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTyrPhe 140  
DB 361 TATAGAGCTCAGACCTGTGGCACTGGAAATTTGCTACTAGATGTGGCTTTGGATA 420  
QY 141 PheSerPheMetThrAnglyPrometIleLeuIleSerAspSerTyrGlnAsnSerThr 160  
DB 421 TTCTCCTTATGACAATGGCCGATGATCTGATTTACAGCTCTTGCGAGATAGACT 480  
QY 161 ThrGluCysGluProGlyPheLeuValbTyrTyrPheAlaLeuProThrSerLeuLeu 180  
DB 481 ACAGAAATGGAACCTGGATTTTAAAGTGGTACTTCTCTCCCTACATCATTAATG 540  
QY 181 GluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200  
DB 541 GAATTCCTGATCCCATCTTTGTTAGTTGCTTATTTGACGCCCATATTACTGGAGCTG 600  
QY 201 TrpValArgGluValbLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220  
DB 601 TGGAAAGCAGAGAACTGAGCAGAGCTGTGCTGAGCACTCTGACTCTGACTCTTCC 660  
QY 221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240  
DB 661 AGCAGTACCAACGACACTCTCTCAGACAGGACCCGATTCAGAGGGGAGACTGCCAGCA 720  
QY 241 ArgValGluThrThrAlaSerLeuGlySerAspLeuSerArgArgIlySerSerLeuLeu 260

Db	721	CGGAAAGAAACACATCGCTCTCTTGGTTACAGCAAGTCAAGAGAAAGGACATCTTTG	780
Qy	261	ProSerIleArgAlaTyrIlysAnsSerAnsValIleAlaSerIlysmcGlyPheLeuSer	280
Db	781	TTTTCCATAGAGCCTACAGAAACGACATGATCGCTCCAAATATGGGCTTCTTCC	840
Qy	281	HisSerAspSerLeuAlaLeuGlnGlnArgIuhIleGluLeuPheArgIlaArgIys	300
Db	841	CACTCAGATTCCTCGCTCTTCAGCAAAAGGAAACATTCAGCACTTTTCAGAGCCAGGAAA	900
Qy	301	LeuAlaIysSerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTyrAlaProCysSer	320
Db	901	TTAGCGCAAGTCATCGGCCCATACTCTTTACACGCTTTTGCCATTTGCTGGGCTCCAAATTC	960
Qy	321	LeuThrThrValIleIleTyrSerPhePheProGluArgAsnLeuThrIysSerThrTyrIyr	340
Db	961	CTGACTACAGTTATATTACTCATTTTTCCTGAAAGAACTGACTTAATCAACCTGGATC	1020
Qy	341	HisThrAlaPheTyrLeuGlnTyrPheAnsSerPheValAsnProPheLeuTyrProLeu	360
Db	1021	CATACTGCGCTTTGGCTCCAGTGGTTCAAATTCCTTTGTAAATCCCTTTTGTATCCATTG	1080
Qy	361	CysHisIysArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgIleSerThr	380
Db	1081	TGTCAACAACGTTTTCAGAGGCTTTCCGAAAAATACCTTCCTGTAGAGGCAATCCACG	1140
Qy	381	ProProHisIleAsnArgSerIleSerThr	389
Db	1141	CCACCACCAACCGCTCAATATACCACT	1167

[illegible]

```

RESULT 4
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US2002098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Alignment Scores:
Pred. No.:      8.77e-138      Length:      1173
Score:          1308.50        Matches:      252
Percent Similarity: 77.52%    Conservative: 48
Best Local Similarity: 65.12%  Mismatches:  84
Query Match:    64.27%        Indels:       3
DB:             9             Gaps:         3

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52  ....
53  ATCCAGGACATCTTAGTGCTTATTTCACATGAATATTATTAGAGCTGTGGAAAGCT 612
Db  .....
QY  204  GluYsLeuSerArgCYaLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db  613  GATCATCTCAGTAGAGGTGCCAAGGCATCTGTGAGCTGACGTGCT---GTCTCTTCCAACATC 669
QY  224  HisGlyHisSerCYaArgGlnAspProAspSerArgAlaThrLeuProAlaArgYsGlu 243
Db  670  TGTGACACCTCATTTCCAGGTAGAGTACTATCTTCAAGAGATCTCTTGTGCATCGACAGA 729
QY  244  ThrThrAlaSerLeuGlySerAspYsSerArgYsSerSerLeuLeuProSerIle 263
Db  730  GTTCCTGCATCTCTTCATTACAGAGACAGAGAGAAAGATAGTCACTAGTTTTCCTCA 789
QY  264  ArgAlaIrrYsAsnSerAsnValIleAlaSerYsMetGlyPheLeuSerHisSerAsp 283
Db  790  AGAACCAAGATGAATATGCAATATCAATTCTTCCAAATGGGTCTCTTCCCAATCGAAT 849
QY  284  SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgYsLeuAlaYs 303
Db  850  TCTGTAGCTCTTCACCAAGGGAACATCTTGAACTGTAGAGCCAGAGATTAAGCCAAG 909
QY  304  SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCYsTrpAlaIleProYsSerLeuThr 323
Db  910  TCACGTGGCATCTCTTAAAGGAGTTTGTGCTGTGTGCTGGGCTCCATATCTCTGTGCCA 969
QY  324  ValIleYrSerPhePhePheProGluArgAsnLeuThrYsSerThrTyrTrpHisIleThrAla 343
Db  970  ATGTGCTTTATTTATTTATCTCTACAGCAACAGGTCTTAATATCAGTTGGTATGAATGCA 1022
QY  344  PheTrpLeuGlnIrrPheAsnSerPheValAsnProPheLeuTyrProLeuCYsHisYs 363
Db  1030  TTTTGGCTTCAGGTGATTCATATCTCTTTGTGCATCTCTTTGTATCCATTTGTGTCAAG 1088

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QY	5	hnsrthrlllealeuthr---SerlleysllserleuthrphleuMeSerleu	23
		::: :::	
Db	13	AATGACAAATCAATTATCTAAGCACTGCTGTACTTACCTAGCATTTTATATGCTTA	72
QY	24	leuallalealleMeleuGlYasnValYalllleuualaphelleValasparg	43
		::: :::	

[illegible]

RESULT 5  
US-09-910-411-1  
Sequence 1, Application US/09910411  
Patent No. US2002137054A1  
GENERAL INFORMATION:  
APPLICANT: Bergsma, Derek  
APPLICANT: Fitzgerald, Laura  
APPLICANT: Li, Xiaorong  
APPLICANT: Michalovich, David  
APPLICANT: Zhu, Yuan  
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor  
FILE REFERENCE: GP70655-2C1  
CURRENT APPLICATION NUMBER: US/09/910,411  
PRIOR FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: 09/693,761  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 09/497,790  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/431,898  
PRIOR FILING DATE: 1999-11-02  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-910-411-1

Alignment Scores:  
Pred. No.: 8,77e-138 Length: 1173  
Score: 1308.50 Matches: 252  
Percent Similarity: 77.52% Conservative: 48  
Best Local Similarity: 65.12% Mismatches: 84  
Query Match: 64.27% Indels: 3  
DB: 9 Gaps: 3

US-10-626-398-10 (1-389) x US-09-910-411-1 (1-1173)

QY	5	AanSerThrlleAlaLeuThr---SerlleYsleSerleuThrpheLeuNecSerleu	23
DB	13	AATAGACACATCAATTAATGACCTAGACCTGCTGTTAGCTTTTATGTCCTTA	72
QY	24	LeuAlaIleAlaIleuSerleuGlyAenValIleValIleuAlaIleAlaIleAlaIle	43
DB	73	GTAGCTTTGCTAATATGCTAGAAATGCTTGCTGCTATTGCTTTGGTGGACAA	132
QY	44	AenLeuArgHisArgSerAnTYrPhePheLeuAenLeuAlaIleAlaIleAlaIle	63
DB	133	AACCTTAGACATCGAAGTAGTATTTTCTTAATGCGCATCTGATCTTTG	192
QY	64	GlyAlaIleAlaIleProleuTYrIleProSerSerleuThrTYrTrpThrSerGly	83
DB	193	GCTGATCTCATCTTCCTTTGTAACATCCCTCACCCCTTGCGAATGGATTTTGGAA	252
QY	84	GlnAlaCysValPheTrpLeuIleThraPyrleuCysThrIleSerValTYrAen	103
DB	253	GAATCTGTGATTTGGCTCACTACTGACTACTGTATCTGTATGACACATCTGTATTA	312
QY	104	IleValIleIleSerTYrAspArgTYrGlnSerValSerAsnAlaValTYrTYrAla	123
DB	313	ATTGCTCATCATGATCATGATCATGATCATGATCATGATCATGATCATGATCATG	372
QY	124	GlnHisSerGlyThrTrpYsIleAlaThrGlnMetValAlaValTYrIlePheSer	143
DB	373	CACACATACGGGGCTCTTGAAGATTGTTACTGATGTCGCTGGGCTGGGCTTC	432
QY	144	MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrgly	163
DB	433	TTAGTCATAGGGGCAATGATCTTCAAGATCTTGAAGATTAAGATGATGATG	492
QY	164	GluProGlyPheLeuYsIleTrpTYrPheAlaLeuProThrSerleuLeuGluPheLeu	183

DB	493	GAACCTGATTTTTCGGAAATGTACATCTTGCCATCATCATCTTGGAAATTCG	552
QY	184	IleProIleLeuLeuValAlaTYrPheSerAlaHisIleTYrTrpSerleuThrpYsArg	203
DB	553	ATCCAGCATCTTATGTCCTTATTTCAACAGAAATTTATGAGCCCTGGAAAGCGT	612
QY	204	GluTYrLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp	223
DB	613	GATCATCTCATAGTAGGCGCAAGCCATCTTGAGACTGACGCT---CTCTTCCAAATC	669
QY	224	HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgYsGlu	243
DB	670	TGTGACACTCATTCAGAGTAGTACTATCTTCAAGAGATCTTCTTCATCAGACAGA	729
QY	244	ThrThrAlaSerleuGlySerAspYsSerArgArgYsSerSerleuLeuProSerIle	263
DB	730	GTTCTGATCTTTCATTCAGAGACGAGAGAGAAAGATGTCATGTTTCTCA	789
QY	264	ArgAlaTYrYsAsnSerAnValIleAlaSerIleYsMetGlyPheLeuSerHisSerAsp	283
DB	790	AGAACCAAGATGATAGCATACATCTGCTTCCAAATGGTTCCTTCCCATCATCAT	849
QY	284	SerleuAlaIleuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgYsleuAlaYs	303
DB	850	TCTGTAGCTCTTCAACAAAGGAAATGTTGAACGCTTAGAGCCAGAGATTAGCCAA	909
QY	304	SerleuAlaIleleuLeuAlaIlePheAlaIleCysTrpAlaProTYrSerleuThrTrp	323
DB	910	TCATGGCCATCTCTTAGGGGTTTGTGCTTGCTGGGCTCCATATCTCTGTTCA	969
QY	324	ValIleTYrSerPhePheProGluArgAenLeuThrYsSerThrTrpYrHisIleAla	343
DB	970	ATTGCTCTTCAATTTATCTCCAGCAACAGATCCCAATACGTTGGATAGAAATGCA	1029
QY	344	PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTYrProleuCysHisIleYs	363
DB	1030	TTTGGCTTCAGTGGTCAATCTTGTGCAATCCCTTTGTATCATCATGATGATGCAAG	1089
QY	364	ArgPheGlnIleAlaPheLeuYsIleLeuProValArgArgGlnSerThrPro---Pro	382
DB	1090	CGCTTCAAAAGGCTTCTTGAATAATTTGTATATAAAAGCAACCTGATCATCA	1149
QY	383	HisAsnArgSerIleSerThr 389	
DB	1150	CACAGTGGTCAATCTTCT 1170	

RESULT 6  
US-09-875-076-13  
Sequence 13, Application US/09875076  
Publication No. US20030017528A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Ruoping  
APPLICANT: Dang, Huang T.  
APPLICANT: Liaw, Chen W.  
APPLICANT: Lin, I-Lin  
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
FILE REFERENCE: AREN0050  
CURRENT APPLICATION NUMBER: US/09/875,076  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 09/417,044  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: 60/120,416  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 60/121,851  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/123,946  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,949  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/136,436  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,437  
PRIOR FILING DATE: 1999-05-28

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PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,293
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-875-076-13

Alignment Scores:
Pred. No.: 8.77e-138 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 10 Gaps: 3

US-10-626-398-10 (1-389) x US-09-875-076-13 (1-1173)
QY 5 AsnSerThrIleAlaLeuThr---SerIleuYsIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATAGCAACAATCAATTTATTCACTAAGCACTCGTGTACTTTAGCATTTTATTTATGTCCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTGCTATATGCTAGGAATGCTTGGTCATTGATTTGCTTTGTGTGACAA 132
QY 44 AsnLeuAlaGlyAspSerAsnThrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAACATCGAAGTATATTTTCTTAACCTGGCCATCTCGACCTCTTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuThrIleProSerSerLeuThrTyThrThSerGlyIys 83
DB 193 GGTGATCTCTCATCTCTTTGATATCCCTCACACGCTGTTGAATGGATTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyIleLeuCysThrAlaSerValTyAsn 103
DB 253 GAAATCTGATTTTGGCTCACTAGCTATCTGTTATGTAAGCATCTGATATTAAC 312
QY 104 IleValIleIleSerTyAspArgTyIleGlnSerValSerAsnAlaValTrpTyArgAla 123
DB 313 ATGTGCTCATCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
QY 124 GlnHisSerGlyThrTrpIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAla 143
DB 373 CAACTACTGGGGCTTGAAGATTTGTTACTCTGATGGGGCCGTTGGGTGCTGGCTTTC 432
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QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGlyCys 163
DB 433 TTAGTAATGGGCCAATATATTCTAGTTCAGAGCTTTGGAAGATGAAGTATGAATGT 492
QY 164 GluProGlyPheLeuIleValTrpTyPheAlaLeuProThrSerLeuLeuGluPheLeu 183
DB 493 GAACCTGATTTTTCGGAATGGAACATCTTCCTGCATCACATCACTTCTGGAATTCG 552
QY 184 IleProIleLeuLeuValAlaIlePheSerAlaHisIleTyTrpSerLeuTrpIysArg 203
DB 553 ATCCAGATCATCTTAGTGGCTTATTTTCAACATGAATTTATTTGAGCCTGTGAAAGCT 612
QY 204 GluIleSerAspGlyLeuSerHisProValLeuProSerAspSerSerAsp 223
DB 613 GATCATCTCAGTAGGTGCAAGCATCTGAGACTGACTGCT--GTCCTTCCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgIleGlu 243
DB 670 TGTGACACTCATTCAGAGTAGACTATCTTCAGAGAGATCTTCTGCAATCGACAGAA 729
QY 244 ThrThrAlaSerLeuGlySerAspIleSerArgIleGlySerSerLeuLeuProSerIle 263
DB 730 GTTCTGCTCATCTTTCATTCAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 789
QY 264 ArgAlaTrpIleAsnSerAsnValIleAlaSerIleMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGAATAGCATATCAATCTCTCCAAATGGTCTCTTCCCAATCAAGT 849
QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgIleLeuAlaIys 303
DB 850 TCTGTAGCTCTTCCCAAGGAACATGTGAACTGTAACGCTTAGAGCCAGAGATTAACCAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaIlePheAlaIleCysTrpAlaProTySerLeuThrThr 323
DB 910 TCACCTGGCATCTCTTGGGCTTTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
QY 324 ValIleTySerPhePheProGluArgAsnLeuThrIleSerThrTrpTyHisThrAla 343
DB 970 ATTGCTTTCAATTTATTTATTCACGACAGACAGAGCTTAATCATGTTGGATGAAATGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyProLeuCysHisIys 363
DB 1030 TTTGGCTTCAGTGGTGAATCTCTTGTCAATCTCTTGTATCCATTTGTGTACAAAG 1089
QY 364 ArgPheGlnIysAlaPheLeuIleLeuProValArgArgGlnSerThrPro--Pro 382
DB 1090 CGCTTTCAAAAGCTTTCTTGAATAATTTGTATATAAAAGCAACCTCTACATCACAA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTCGTCAGTATCTTCT 1170

RESULT 7
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
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1	PRIOR FILLING DATE: 1998-10-13	
2	PRIOR APPLICATION NUMBER: 60/110,066C	
3	PRIOR FILLING DATE: 1998-11-27	
4	PRIOR APPLICATION NUMBER: 60/120,416	
5	PRIOR FILLING DATE: 1999-02-16	
6	PRIOR APPLICATION NUMBER: 60/121,852Z	
7	PRIOR FILLING DATE: 1999-02-26	
8	PRIOR APPLICATION NUMBER: 60/109,213	
9	PRIOR FILLING DATE: 1998-11-20	
10	PRIOR APPLICATION NUMBER: 60/123,944AA	
11	PRIOR FILLING DATE: 1999-03-12	
12	PRIOR APPLICATION NUMBER: 60/123,945S	
13	PRIOR FILLING DATE: 1999-03-12	
14	PRIOR APPLICATION NUMBER: 60/123,946B	
15	PRIOR FILLING DATE: 1999-03-12	
16	PRIOR APPLICATION NUMBER: 60/123,949A9	
17	PRIOR FILLING DATE: 1999-03-12	
18	PRIOR APPLICATION NUMBER: 60/152,524A	
19	PRIOR FILLING DATE: 1999-09-03	
20	PRIOR APPLICATION NUMBER: 60/151,114A	
21	PRIOR FILLING DATE: 1999-08-27	
22	PRIOR APPLICATION NUMBER: 60/108,029P	
23	PRIOR FILLING DATE: 1998-11-12	
24	PRIOR APPLICATION NUMBER: 60/136,436E	
25	PRIOR FILLING DATE: 1999-05-28	
26	PRIOR APPLICATION NUMBER: 60/136,439P	
27	PRIOR FILLING DATE: 1999-05-28	
28	PRIOR APPLICATION NUMBER: 60/136,567P	
29	PRIOR FILLING DATE: 1999-05-28	
30	PRIOR APPLICATION NUMBER: 60/137,127P	
31	PRIOR FILLING DATE: 1999-05-28	
32	PRIOR APPLICATION NUMBER: 60/137,131H	
33	PRIOR FILLING DATE: 1999-05-28	
34	PRIOR APPLICATION NUMBER: 60/141,448B	
35	PRIOR FILLING DATE: 1999-06-29	
36	PRIOR APPLICATION NUMBER: 60/136,437P	
37	PRIOR FILLING DATE: 1999-05-28	
38	PRIOR APPLICATION NUMBER: 60/156,555S	
39	PRIOR FILLING DATE: 1999-09-29	
40	PRIOR APPLICATION NUMBER: 60/156,634A	
41	PRIOR FILLING DATE: 1999-09-29	
42	PRIOR APPLICATION NUMBER: 60/156,653C	
43	PRIOR FILLING DATE: 1999-09-29	
44	PRIOR APPLICATION NUMBER: 60/157,280B	
45	PRIOR FILLING DATE: 1999-10-01	
46	PRIOR APPLICATION NUMBER: 60/157,294A	
47	PRIOR FILLING DATE: 1999-10-01	
48	PRIOR APPLICATION NUMBER: 60/157,291I	
49	PRIOR FILLING DATE: 1999-10-01	
50	PRIOR APPLICATION NUMBER: 60/157,282Z	
51	PRIOR FILLING DATE: 1999-10-01	
52	PRIOR APPLICATION NUMBER: 60/156,633C	
53	PRIOR FILLING DATE: 1999-09-29	
54	NUMBER OF SEQ ID NOS: 146	
55	SOFTWARE: PatentIn version 3.0	
56	SEQ ID NO 13	
57	LENGTH: 1173	
58	TYPE: DNA	
59	ORGANISM: Homo sapiens	
60	US-09-876-252-13	
61	Alignment Scores:	
62	Pred. No.:	8.77e-138
63	Scores:	1308.50
64	Percent Similarity:	77.52%
65	Best Local Similarity:	65.12%
66	Query Match:	64.27%
67	DB:	10

US-10-626-398-10 (1-389) x US-09-876-252-13 (1-1173)

QY	5	AanSerThrllealeuThr--SerllelyslleSerleuThrPheleuMeSerleu	23
Db	13	AATAGCAACAATCAATTTATCTACTAAGCACTGGTGTACTTAGCAATTTTATGCTTCA	72
QY	24	LeuAlaIleAlaIleMetleuGlyAsnValValAlIleLeuAlaPheIleValAspArg	43
Db	73	GTAGCTTTTGGTAAATAGCTAGAAAGCTTTGGCATTTTAAAGCTTTTGGTGGACAA	132
QY	44	AsnLeuArgHisArgSerAsnThrPhePheLeuAsnLeuAlaIleAlaAspPheVal	63
Db	133	AACTTGAACATCGAAGTAGTATTTTCTTTAACTTGGCACTCTGACTCTTTGTG	192
QY	64	GlyAlaIleAlaIleProleuTyrlleProSerSerleuThrTyrlPheSerGlyAs	83
Db	193	GGTGGATCTCCATCTCTTTGTAACCTCCCTCACAGCTGTTGCAATGGGATTTGGAAAG	252
QY	84	GlnAlaCysValPheTrpLeuIleThrAspTyrlleuLeuGlyTrnAlaSerValTyrsn	103
Db	253	GAAATCTGTGTATTTGGCTCAGTACAGCATCTGTATGTATACAGCATCTGTATATAC	312
QY	104	IleValleuIleSerTyrrAspArgTyrlGlnSerValSerAsnAlaValTyrrArgAla	123
Db	313	ATTGTCTTCATCAGCTATGATGATGATCTGCTGATCTTAATGCTGTCTTATGAACT	372
QY	124	GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe	143
Db	373	CAACATCTGGGGCTTGAAGATTTGTAATCTGTGATGGTGGCGCTTGGGCTGGCTTC	432
QY	144	MetThrAsnGlyProMetIleleuIleSerAspSerTrpGlnAsnSerThrThiGlyCys	163
Db	433	TTAGTGATGGCCAAATGATTCGTATTCAGATCTTGGAAAGATGAAAGTAGTGAAGT	492
QY	164	GluProGlyPheLeuLysValTrpTyrlPheAlaLeuProThrSerleuLeuGlnPheLeu	183
Db	493	GAACTGGATTTTTTGGGAATGGATACCTCTGGCATCACATCATCTTGGAAATTCGTG	552
QY	184	IleProIleLeuLeuValAlaIleTyrrPheSerAlaHisIleTyrrTrpSerleuTrpLysArg	203
Db	553	ATCCAGATCACTTAGTGGCTTATTTTCAACATGAATATTATTTGGAGCTGTGGAAAGGT	612
QY	204	GluLysIleuSerArgCysLeuSerHisProValleuProSerAspSerSerSerAsp	223
Db	613	GATCATCTCAGTAGAGTGGCAAGGCATCTGAGTGACTCT--GTCCTTCCAAACATC	669
QY	224	HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysLeu	243
Db	670	TGTGGACACTATTCAGAGTAGACTATCTTCAAGAGATCTTTCTGATCGACAA	729
QY	244	ThrThrAlaSerleuGlySerAspLysSerArgTyrlGlySerSerleuLeuProSerIle	263
Db	730	GTCTCTGATCTCTTCATTCAGAGACAGACAGAGAAAGTAGTCTCATGTTTCTCCA	789
QY	264	ArgAlaTyrlLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp	283
Db	790	AGAACAAGATGATAGCAATACATGCTTCCAAATAGGGTCTCTTCCCAATCAGAT	849
QY	284	SerleuAlaLeuGlnGlnArgGlnHisIleGlyLeuPheArgAlaArgLysLeuAlaLys	303
Db	850	TCTGTAGCTTTCACCAAGAGGAACATGTTGTAAGCTCTTAAAGCAGAGATTTAGCCAAAG	909
QY	304	SerleuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrrSerleuThrThr	323
Db	910	TCACTGGGCATCTCTTAGGGGTTTTGCTGTGTGCTGGGCTCCATATCTCTGTCCA	969
QY	324	ValIleTyrrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrrHisAla	343
Db	970	ATTGTCCTTCATTTTATCTCTGACAAACAGCTCTTAATCAGTTTGGTATAGAAATGCA	1029
QY	344	PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrrProLeuCysHisLys	363
Db	1030	TTTGGCTTCAAGTGTCAATCTCTTGTGCATCTCTTTGGTATCAATGTGTGCACAG	1089

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QY 364 ArgPheGlnIlySAIAPheLeuYsileuProValArgArgGlnSerThrPro---Pro 382
DB 1090 CGCTTCAAAAGCGCTTCTTGAAAATATTTGTATATAAAAGCAACCTTACACACAA 1149
QY 383 HisAenArgSerIleSerThr 389
DB 1150 CACAGTCGTCAGTATCTTCT 1170

RESULT 8
US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1

Alignment Scores:
Pred. No.: 8,776-138 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
DB: 13 Gaps: 3

US-10-626-398-10 (1-389) x US-10-052-193-1 (1-1173)
QY 5 AenSerThrIleAlaLeuThr---SerIleYsileuSerLeuThrPheLeuMetSerLeu 23
DB 13 AATACACACATCAATTAATTAACCTAGCACTCGTGTACTTACATTTTATATGTCCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAenValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTTGCTATATATGCTAGGAATGCTTTGGTCATTTTACCTTTTGTGTGACAA 132
QY 44 AenLeuAIGHIArgSerAenTYrPhePheLeuAenLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGCCATCTCGACTTCTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuTYrIleProSerSerLeuThrTYrThrSerGlyAs 83
DB 193 GGTGTGATCTCCATTCCTTGTACATCCCTCAACGCGTGTGAATGGGATTTTGGAAAG 252
QY 84 GlnAlaCysValPheTYrPheLeuIleThrAspTYrLeuLeuCysThrAlaSerValTYrAsn 103
DB 253 GAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGACGACATCTGTATATAC 312
QY 104 IleValIleuIleSerTYrAspArgTYrGlnSerValSerAenAlaValTYrTYrArgAla 123
DB 313 ATGTGCTTCATCAGCTATGATCGATACCTGACAGTCTCAAAATGCTGTCTTATAGAACT 372
QY 124 GlnHisSerGlyThrTYrPheValIleAlaThrGlnMetValAlaValTYrIlePheSerPhe 143
DB 373 CACCACTACGGGGCTTGAAGATGTGTACTCTGATGGTGCGGTGGTGGCTGCGCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTYrGlnAsnSerThrThrGluCys 163
DB 433 TTAGGGAATGGGCAATGATTTCTAGTTTCAGAGCTCTTGGAAGAGTGAAGTGAATGT 492
QY 164 GluProGlyPheLeuYsileuTYrPheAlaLeuProThrSerLeuLeuGluPheLeu 183

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DB 493 GAACCTGATTTTTTCGAAATGTATACCTTGCCATCACATCATCTTGGAATTCGTG 552
QY 184 IleProIleLeuLeuValAlaTYrPheSerAlaHisIleTYrTrpSerLeuTrpYsArg 203
DB 553 ATCCAGCATCTTATGCTGCTTATTTTCAACATGATATTTATGAGCTGTGGAAAGCT 612
QY 204 GluYsLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAGTAGAGGTGCNAAGCCATCTGAGACTGACTGCT---GTCCTTCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgYsGlu 243
DB 670 TGTGACACTATTCAGAGTAGAATATCTTCAAGAGATCTCTTCTGCAACGACAGA 729
QY 244 ThrThrAlaSerLeuGlySerAspYsSerArgYsSerGlySerSerLeuLeuProSerIle 263
DB 730 GTTCTGCAATCTTTCATTCACAGAGACAGAGAGAGAAAGATAGTCTATGTTTCTTCA 789
QY 264 ArgAlaTYrYsAsnSerAenValIleAlaSerIysMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGATATGCAATATCAATGCTTCCAAATGGGTTCTTCTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnArgGlnArgHisIleGluLeuPheArgAlaArgYsLeuAlaYs 303
DB 850 TCTGTAGCTCTTCACCAAGGAACATGTGAACGCTTAGAGCCAGAGATTAACCAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTYrSerLeuThrThr 323
DB 910 TCACGTGCAATTCCTTCTTGGGGTTTTCCTGTTCTGTGCTGAGCTCCATATCTTCTGTACA 969
QY 324 ValIleTYrSerPhePheProGluArgAenLeuThrYsSerThrTYrTrpHisThrAla 343
DB 970 ATTGCTTCATTTATTTATTCCTCAGACACAGGTCCCTAATATCGTTGATATGAAATGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAenProPheLeuTYrProLeuCysHisYs 363
DB 1030 TTTTGCTTCAGTGGTTCATATTCCTTGTGCAATCTCTTGTATCCATTTGTGTACAAAG 1089
QY 364 ArgPheGlnIlySAIAPheLeuYsileuProValArgArgGlnSerThrPro---Pro 382
DB 1090 CGCTTCAAAAGCGCTTCTTGAAAATATTTGTATATAAAAGCAACCTTACACACAA 1149
QY 383 HisAenArgSerIleSerThr 389
DB 1150 CACAGTCGTCAGTATCTTCT 1170

RESULT 9
US-10-272-983-13
; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28

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; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13

Alignment Scores:
Pred. No.:      8,77e-138      Length:      1173
Score:          1308.50       Matches:      252
Percent Similarity: 77.52%    Conservative: 48
Best Local Similarity: 65.12%  Mismatches:   84
Query Match:    64,274       Indels:       3
DB:             15           Gaps:         3

US-10-626-398-10 (1-389) x US-10-272-983-13 (1-1173)
QY 5 AasnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATAGCAATCAATTAATTAATCACTGAGTGTGTTAGCATTTTATGCTCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTTGCTTAATAGTGAAGAAATGCTTGCTATTAGCTTTTGAGTGAGCAAA 132
QY 44 AsnLeuArgHisArgSerAsnIlePhePheLeuAsnLeuAlaIleAlaPhePheVal 63
DB 133 AACCTTAGACATGAGTACTATTATTTTCTTAACCTGACATCTCTGCTTTGTG 192
QY 64 GluAlaIleAlaIleProLeuIleProSerSerLeuThrIleProSerGlyLeu 83
DB 193 GGTGTGCTCTCATCTCTTTGACATCCCTCACACGGTGTGCGAATGGATTGGAAAG 252
QY 84 GluAlaCysValPheTrpLeuIleIleAspIleLeuLeuCysThrAlaSerValIleAsn 103
DB 253 GAATATCGTATATTGGCTCACTACGACTATCTGTATGACAGATCTGTATATAC 312
QY 104 IleValIleLeuSerIleAspArgIleGlnSerValSerAsnAlaValIleIleArgAla 123
DB 313 ATGTCTCTCATGAGTATGATGATCACTGCTCAATGCTGTGCTTATAGAACT 372
QY 124 GlnHisSerGlyThrTrpIleAlaIleThrGlnMetValAlaIleIlePheSerPhe 143
DB 373 CAACATACCTGGGCTCTTGAAGATTGTACTGATGATGGCCCTTTGGGCTGGCCCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpIleAsnSerThrIleGluCys 163
DB 433 TTAGTGAATGGCCCATGATTTCAAGTCTTGAAGATGAGTGAATGAT 492
QY 164 GluProGlyPheLeuLysIleTrpIlePheAlaLeuProThrSerLeuGluPheLeu 183
DB 493 GAACCTGATTTTTCGAAATGATGATCTTCCATCAATCATCTTGAATTCGTG 552
QY 184 IleProIleLeuLeuValAlaIleTrpPheSerAlaHisIleIleTrpPheSerLeuTrpIleArg 203
DB 553 ATCCCACTCATTTAGTGGCTTATTTTCAACATGAATTTTATGAGACCTGTGAGCGGT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTGATGATGCCAAGGCATCTGAGTGAATGCT---GTCTCTTCCAAATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrIleuProAlaIleGlyGln 243
DB 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTTTCGATCGACAGAA 729
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QY 244 ThrThrAlaSerLeuGlySerAspIleAspIleArgIleSerSerLeuProSerIle 263
DB 730 GTTCCCTGCATCTTTCATTTACAGAGACAGAGAGAAAGTACTCATGTTTCTCTCA 789
QY 264 ArgAlaIleTrpLysAsnSerAsnValIleAlaSerIleMetCylPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGAATGACATATACATTTGCTCCAAATGGGTTCTCTTCCATCAGAT 849
QY 284 SerLeuAlaIleGlnIleGlnArgGlnIleGlnLeuPheArgAlaIleArgLysLeuAlaIle 303
DB 850 TCTGTAGCTCTTACCAAGGAAACAGTTGAATCTGTAGACCCAGAGATTAAGCCAAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaIleAlaPheAlaIleCysTrpAlaProIleSerLeuThr 323
DB 910 TCATGCGCATTTCTCTTAGGCGGTTTGTGCTGTTGCTGGCTGCATATTTCTGTTGACA 969
QY 324 ValIleTrpSerPhePheProGluArgAsnLeuThrLysSerThrTrpIleHisThrAla 343
DB 970 ATGTGCTTCATTTATTTCTCAGCAACAGTCTTAATCACTTTGGTATGAATTTGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuIleProLeuCysHisLys 363
DB 1030 TTTTGCTTCAGTGTTCATTTCTTTGTCAATCTCTTTGTATCCATTTGTGCACAA 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgGlnSerThrPro---Pro 382
DB 1090 CGCTTTCAAAGGCTTTCTTGAAATATTTTGTATATAAAGCACTCATCATCAACAA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACATCGGTCACTATCTTCT 1170

RESULT 10
US-10-354-769-1
; Sequence 1, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: P010373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1

Alignment Scores:
Pred. No.:      8,77e-138      Length:      1173
Score:          1308.50       Matches:      252
Percent Similarity: 77.52%    Conservative: 48
Best Local Similarity: 65.12%  Mismatches:   84
Query Match:    64,274       Indels:       3
DB:             15           Gaps:         3

US-10-626-398-10 (1-389) x US-10-354-769-1 (1-1173)
QY 5 AasnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATAGCAATCAATTAATTAATCACTGAGTGTGTTAGCATTTTATGCTCTTA 72
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QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTTGCATATATGCTAGAGAAATGTTGGTCACTTTTGTGTGGACAAG 132
QY 44 AsnLeuAArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGTAGATATTTTCTTAATCTGGCATCTGACCTCTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyAs 83
Db 193 GGTGGATCTCCATTCCTTTGTACATCCCTCACAGCGCTTGGATGGGATTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
Db 253 GAAATCTGGTATTTTGGCTCACTGACTGACTATCTGTTATGACAGCATCTGATATTAAC 312
QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
Db 313 ATGTGCTCATCAGCATATGATGATACCTGACAGTCTCAAAAGCTGTCTTATAGAACT 372
QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db 373 CAACATCTGGGCTCTTGAGATTTGTTACTCTGATGAGTGGCGTTGGGTGGCTGCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGlyCys 163
Db 433 TTAGTGAAATGGGCAATGATTTCTAGATTTCAGAGTCTGGCAAGATGAGTAGTGAAT 492
QY 164 GluProGlyPheLeuLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACCTGGATTTTTCGGAATGATACATCTTGCATCATCTTCTTGGAAATTCGCG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
Db 553 ATCCAGTATCTTATGTCCTTATTTTCAACATGAAATTTATTTAGAGCTTGGAAGCT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGAGGCGCAAGAGCCATCTGAGTCACTGCT---GTCCTTCCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerHisArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGACACTCATTCAGAGTAGACTATCTTCAGAGAGATCTCTTCTGACATCGACAGA 729
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgGlySerSerLeuLeuProSerIle 263
Db 730 GTTCTGCTGATCTTTCATTCACAGACACAGAGAGAGAGATGCTCATGTTCCTCA 789
QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGATATGCAATCAATTCCTCAAAATGGTTCCTTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGAGAGCTTTCACCAAGGAGAACTGTGAACTGCTTAGAGCCAGGAGATTAAGCAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
Db 910 TCACCTGGCATCTCTTACGGGCTTTTGTCTGTTGCTGGGCTCCATATCTCTGTTCA 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
Db 970 ATTGTCCTTCAATTTATTCCTCACACACAGGCTCAATATCAGTTGATATGAATGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
Db 1030 TTTTGGCTTCAGTGTCAATTCCTTGTCAATCCCTTTTGTATCCATTTGTGTACAG 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
Db 1090 CCGTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAGACCTTACATCACAA 1149
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QY 383 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGTCAGTATCTTCT 1170

RESULT 11
US-10-393-807-13
/ Sequence 13, Application US/10393807
/ Publication No. US20030175891A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
/ FILE REFERENCE: AREN0050
/ CURRENT APPLICATION NUMBER: US/10/393,807
/ PRIOR APPLICATION NUMBER: US/09/417,044
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-393-807-13

Alignment Scores:
Pred. No.: 8,77e-138 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
Gaps: 3
DB: 16

US-10-626-398-10 (1-389) x US-10-393-807-13 (1-1173)
QY 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATACACATCAATATTATTCACAGCACTCCTGTTACTTATGCAATTTTATGTCCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTTGCATATATGCTAGAGAAATGTTGGTCACTTTTGTGTGGACAAG 132
QY 44 AsnLeuAArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGTAGATATTTTCTTAATCTGGCATCTGACCTCTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyAs 83
Db 193 GGTGGATCTCCATTCCTTTGTACATCCCTCACAGCGCTTGGATGGGATTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
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Db	253	GAACCTGCTGATTTTGGCTACTACTACTGACTATCTGTTATGACAGCATCTGTATATTAAC	312
Qy	104	lIeValIeuIIeSeTyraSpAqTgYrGInSeRValSeRaSnAlaValTPrYrAqAla	123
Db	313	ATTGCTCATCAGCTATGATGATGATACCTGCTCAGTCTCAAAAGCTGTGTCTTATAGAACT	372
Qy	124	GlInHIsSeRgYlThTPrYsIleAlaThrGInMeTValAlaValTPrIlePheSeRPhE	143
Db	373	CAACtACTGAGGGCTTGAGAGTGTACTCGATGGAGTGGCCGTGTGGGTGCTGGCCCTTC	432
Qy	144	MeTThraNgYlProMeTlIeUleIIeSeRaSpSeRTPGInaSnSeRThrThrGInUcYs	163
Db	433	TTAGGAAATGGGCCAATGATTTCTAGTTCTCAGAGTCTTGAGAGGATGAAAGATGTAATGT	492
Qy	164	GlUpProGIlPhELeuLylUySTPrYrPhEaIaLeuProThrSeRleuGluPhELeu	183
Db	493	GAACCTGATTTTTTTCGGAATGGTAACATCCCTGGCATCAGATCATCTTGGAAATTCGGG	552
Qy	184	lIePProIleUleuValAlaTyRPhSeRaIahIsIleTyTTPSeRleuTPrYsAqg	203
Db	553	ATCCAGACTCTTATGTCGTATTTTCAACGAATATTTATTTGAGCTGTGGAAAGGCT	612
Qy	204	GlUySeLSeuSeRArXCYeLeuSeRthIProValLeuProSeRaSpSeRSeSeRaSp	223
Db	613	GATCATCTCAGTAGGTGCCAAAGCCATCCTGGACTGACTGCT--GTCCTTCAACATC	669
Qy	224	HISeGIlHIsSeRCySaRgGInaSpProaPSeRaIgaIaThrLeuProAlaRgYleGlu	243
Db	670	TGTGGACACTATTGAGAGTAGACTATCTTCAAGAGATCTCTTTCGATCCAGACAGA	729
Qy	244	ThrThraIaSeRleuGlySeRaSpIySeRaRgArGlySeSeSeRleuSeuProSeRle	263
Db	730	GTTCCCTGATCTCTTCACTCAGAGAGACAGAGAAAGATGATCTCATGTTTCTTCA	789
Qy	264	ArgAlaTyRlySaSnSeRaSnValIleIaSeRlySmEgYlPhELeuSeRthISeRaSp	283
Db	790	AGAACCAAGATGAATAGCAATACAAATTCCTCCAAAGGGTCTCTCCCAATCAAGT	849
Qy	284	SeRleuAlaLeuGInGInARgIuHIsIleGInleuPheARgAlaARgYleuAlaYs	303
Db	850	TCTGTAGCTCTTCAACCAAGGAACTGTGAACGTCTTAGAGCCAGAGATGATCCAAAG	909
Qy	304	SeRleuAlaIleLeuLeuAlaIaPheAlaIleCYsTPAlaProTySeRleuThrThr	323
Db	910	TCACGTGGCATTCCTTAGAGGGTCTTGTCTGTCTGGGCTCCATATTCCTGTTCACA	969
Qy	324	ValIleTyRSeRPhEProGluARgAnleuThrlySeRThrTPrYrHIsThrAla	343
Db	970	ATTGTCCCTTCAATTTATTTCTCAGCAACAAGCTCCTAAATCACTTGTGTATAGAAATTC	1023
Qy	344	PhETPrIeUGInTPRPhASnSeRPhEValaSnProPheLeuTyRProUcYHIsIlyS	363
Db	1030	TTTGGCTTCAGTGGTGTCAATTCCTTTGTCAATCTCTTTGTATCAATGTGTACAAAG	1088
Qy	364	ARgPheGInlySaIaPheLeuYsIleUeProValaARgARgInSeRThrPro--Pro	382
Db	1090	CGCTTTCAAAAGGCTTCTTGAAATATTTGTATAAAAAAGCAACCTCTACATCACAA	1145
Qy	383	HIaSnARgSeRleSeRThr 389	
Db	1150	CACAGTCCGTCAGTATCTTCT 1170	
RESULT 12			
US-10-417-820A-13			
; Sequence 13, Application US/10417820A			
; Publication No. US20030229216A1			
; GENERAL INFORMATION:			
; APPLICANT: Chen, Ruoping			
; APPLICANT: Liaw, Ruoping			
; APPLICANT: Lowitz, Kevin			
; APPLICANT: Chalmers, Derek T.			
; APPLICANT: Behan, Dominic P.			

```

; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-13

Alignment Scores:
Pred. No.:      8, 77e-138      Length:      1173
Score:          1308.50        Matches:     252
Percent Similarity: 77.52%    Conservative: 48
Best Local Similarity: 65.12%  Mismatches:   84
Query Match:    64.27%       Indels:      3
DB:             17            Gaps:         3

US-10-626-398-10 (1-389) x US-10-417-820A-13 (1-1173)
QY      5 AsnSerThrIleAlaLeuThr--SerIleuylSeSerLeuThrPheLeuMetSerLeu 23
Db      13 AATAGCAACATCATTTATTACTACTAGACGCTGTGTACTTATAGCATTTTATTCCTTA 72
QY      24 LeuAlaIlleAlaMetLeuGllyAsnValValAlIleuAlaPheIleValAspArg 43
Db      73 GTGGCTTTTGCTATATGCTTAGGAATCCTTGGTCATTTAGCTTTGGTGGGACAA 132
QY      44 AsnLeuArgHisArgSerAntyrRhePheLeuMetLeuAlaIleAlaaspPhePheVal 63
Db      133 AACCTTAGACATCGAAGAAGTATATTTTTTTCTTAACCTGGGCATCTCGACTCTTTGTG 197
QY      64 GlValAlaIleAlaIleProLeuTyrlleProSerSerLeuThrTyrrTPThrSerGIlyls 83
Db      193 GGCTGTATCTCATTTCTTGTATCCATCCCTCACACGCTGTTGCAATGGATTTTGGAAAG 255
QY      84 GlAlaICysValPheTrpLeuIleThrAspyrIleuLeuCystrAlaIaservalTyraSn 103
Db      253 GAATCTGTGTATTTTGGCTCACTACTGACATCATCTGTATATGACGATCTGTATATAC 312
QY      104 IlleValleuIleSerTyrrAspArgtyrGlnSerValSerAsnaIaValITryrArgAla 123
Db      313 ATGTCTCATACGCTATGATGATGATACCTGTACGTCATAATATGCTGTCTTATAGACT 372
QY      124 GlNHisSerGIyThrTrpIlylIleAlaThrGlnMetValAlaValITrpIlePheSerPhe 143
Db      373 CAACATACCTGGGCTCTTGAAAGATTGTACTCTGAATGGTGGCCGTTTGGGTGCTGCCCTTC 432
QY      144 MetThrAsnGlyProMetIleLeuIleSerAspSerITyrlAsnSerThrGluCys 163

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Db 433 TTAGTGAAGGGCCCAATGATTTCTAGTTTCAGAGTCTTGAGAGATCAAGATGATGTAATGT 492
Oy 164 GIUPROGILPheLeuLysTrpTyRPhaAlaLeuProThrSerLeuLeuLysLeu 183
Db 493 GAACCTGGATTTTTCGGAATGTGTACATCTTCCATCATTCTTGGAAATTCGTG 552
Oy 184 ILeProIleLeuLeuValAlaTyRPhaSerAlaHisIleTyRTrpSerLeuTrpLysArg 203
Db 553 ATCCAGATCATCTTATGCTTATTTCAACATGATATTATTATTTGAGCCTGTGAGAGCGT 612
Oy 204 GIULYSLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGAGTGCACAAAGCCATCTGACATGACATGCT---GTCTCTTCAACATC 669
Oy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProLysArgLysGlu 243
Db 670 TGTGACACTCATTCAGAGTAGACTATTTCAAGAGATCTCTTCTTCACATCGACAGAA 729
Oy 244 ThrThrAlaSerLeuGlySerAspLysSerArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCCGATCTCTTTCATTCACAGAGACAGAGAGAAAGTAGTCTCATGTTTCTCTCA 789
Oy 264 ArgAlaTyRlysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AAGAACCAAGATGAATAGCAATACAAATGTCTTCCAAATGGGTCTCTCCCAATCAGAT 849
Oy 284 SerLeuAlaLeuGlnGlnArgLysHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGCTCTTCCACCAAGGAGACATGTGAACTCTTAGAGCCAGAGATTAAGCCAG 909
Oy 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
Db 910 TCACGTGGCCATCTCTTACGGGTTTGTCTGTGGTGGCTCCATATCTCGTTACACA 969
Oy 324 ValIleTySerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
Db 970 ATGTGCTTTCATTTTATCTCTCAGCAGACAGGCTCTAAATCAGTTGTGATAGAAATGCA 1029
Oy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyRProLeuCysHisLys 363
Db 1030 TTTTGGCTTCAGTGTGTTCAATCTTGTCAATCTCTTTGTATCCATGTTGTGTACAG 1089
Oy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
Db 1090 CCCTTTCAAAAGGCTTCTTGAATAATTTGTATAAAAGCAACCTCACCATCACA 1149
Oy 389 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 13
US-10-349-253A-1
; Sequence 1, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Graybill, Todd
; APPLICANT: Li, Xiaolong
; APPLICANT: Michalovich, David
; APPLICANT: Morrow, Dwight
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C2
; CURRENT APPLICATION NUMBER: US/10/349,253A
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/910,411
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/593,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
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; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-349-253A-1

Alignment Scores:
Pred. No.: 8.77e-138 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.52% Conservative: 48
Best Local Similarity: 65.12% Mismatches: 84
Query Match: 64.27% Indels: 3
Dels: 18 Gaps: 3

US-10-626-398-10 (1-389) x US-10-349-253A-1 (1-1173)
Oy 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCAACAATCAATTTATCTAGACACTGCTGTTACTTTAGCATTTTATATGCTTCA 72
Oy 24 LeuAlaIleAlaIleMetLeuGlyAsnValAlaValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTGCTATATATCTAGAAATGCTTTGTCATTTTATGCTTTTGTGTGACAGAA 132
Oy 44 AsnLeuAlaGHisArgSerAsnTyRPhaPheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTACACATCGAAGTAGATATTTTCTTAATCTGGCCATCTGACTCTGACTCTTGTG 192
Oy 64 GlyAlaIleAlaIleProLeuTyRLeProSerSerLeuThrTyRTrpThrSerGlyLys 83
Db 123 GGTGATCTCTCATCTCTTGTGTACTTCCCTCACAGCGCTTGAATGGATTTTGGAAAG 252
Oy 84 GlnAlaCysValPheTrpLeuIleThrAspTyRLeuLeuCysThrAlaSerValTyRAsn 103
Db 253 GAAATCTGTATATTTTGGCTCAGTACTGACTATCTGTTATGTACAGCATCTGTATATAC 312
Oy 104 ILeValLeuIleSerTyRAspArgTyRAsnValSerAsnAlaValTrpTyRArgAla 123
Db 313 ATGTGCTTCATCAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
Oy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db 373 CAACATCTGGGCTTGAAGATTTCTACTGATGTGTGGCGCTTGTGGCTGTGGCTTTC 432
Oy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGlyCys 163
Db 433 TTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAGATGAAAGTAGTAATGT 492
Oy 164 GIUPROGILPheLeuLysTrpTyRPhaAlaLeuProThrSerLeuLeuLysLeu 183
Db 493 GAACCTGGATTTTTCGGAATGTGTACATCTTCCATCATTCTTGGAAATTCGTG 552
Oy 184 ILeProIleLeuLeuValAlaTyRPhaSerAlaHisIleTyRTrpSerLeuTrpLysArg 203
Db 553 ATCCAGATCATCTTATGCTTATTTCAACATGATATTATTATTTGAGCCTGTGAGAGCGT 612
Oy 204 GIULYSLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGAGTGCACAAAGCCATCTGACATGACATGCT---GTCTCTTCAACATC 669
Oy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProLysArgLysGlu 243
Db 670 TGTGACACTCATTCAGAGTAGACTATTTCAAGAGATCTCTTCTTCACATCGACAGAA 729
Oy 244 ThrThrAlaSerLeuGlySerAspLysSerArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCCGATCTCTTTCATTCAGAGAGACAGAGAGAAAGTAGTCTCATGTTTCTCTCA 789
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QY 264 ArgAlaTyrIleAsnSerAsnValIleAlaSerIleMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGATGACATATGCTTCCAAATGGGCTCTTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgIleValAlaVal 303
DB 850 TGTGTAGCTCTTCCAAAGGGAACATGTTGAATCTGTTAGACCAGAGAAATTAGCCAAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaIlePheAlaIleCysThrAlaProIleSerLeuThrThr 323
DB 910 TCACGTGCCATCTCTTACGGGCTTTTGTGCTTGTGCTGCTCATATTTCTCTGTTCACA 969
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrIleSerThrTyrTrpHisThrAla 343
DB 970 ATGTGCTTTCATTTATTTCTCAGACACAGTCCCAATCAGTTTGATAGATTGCA 1029
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisIleVal 363
DB 1030 TTTTGGCTTCAGAGGTCAATTCCTTTGTCAATCTCTTTGTATCATTTGTGTCCAAAG 1089
QY 364 ArgPheGlnIleValPheLeuIleValIleLeuProValArgArgIleSerThrPro---Pro 382
DB 1090 CGCTTTCAAAGGCTTTCTTGAAATATTTTGTATATAAAGCAACCTTACCATCACA 1149
QY 383 HisAsnArgSerIleSerThr 389
DB 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 14
US-10-723-955-13
Sequence 13, Application US/10723955
Publication No. US20040110238A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmer, Derek T.
APPLICANT: Lin, I-Lin
APPLICANT: Liao, Chen W.
APPLICANT: Lehman-Bruinsma, Karlin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huang T.
APPLICANT: Chen, Kuoping
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: 7.US29.CON
CURRENT APPLICATION NUMBER: US/10/723,955
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 10/417,820
PRIOR FILING DATE: 2003-4-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 1173
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-955-13

Alignment Scores:
Pred. No.: 8,776-138
Score: 1308.50
Percent Similarity: 77.52%
Best Local Similarity: 65.12%
Query Match: 64,278
DB: 19 Gaps: 3

US-10-626-398-10 (1-389) x US-10-723-955-13 (1-1173)

QY 5 AsnSerThrIleAlaLeuThr---SerIleValIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATAGCAATCAATTAATTAATCACTAGACACTGGTACTTACATTTTATGCTTCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValIleValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTGCTATATATGCTAGGAATGCTTGGTCAATTTTACCTTTGTGTGACAA 132
QY 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAGACATGAGATGATATTTTCTTAATCTGGCCATCTCTGCTTCTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpHisSerGlyIle 83
DB 193 GGTGATCTCCATCTCTTGTATCATCTCCACACGCTGTCGAATGGATTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpPheIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
DB 253 GAATGTGTATTTTGGCTCACTAGCTATCTGTATATGACACATCTGTATATAC 312
QY 104 IleValIleLeuSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrIleArgAla 123
DB 313 ATGTGCTCATCGATATGATCATCTGCTGAGTCTCAATGCTGTGTATTAAGACT 372
QY 124 GlnHisSerGlyThrTrpIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 373 CACATATCGGGGCTTGAAGATGTTACTCTGATGAGCGGCTTGGGGCTGGCCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGluCys 163
DB 433 TTAGTAATGGGCAATGATTTCTAGTTCAAGTCTTGAAGATGAGATGATGATGT 492
QY 164 GluProGlyPheLeuIleValTyrPheAlaLeuProThrSerLeuGluPheLeu 183
DB 493 GAACCTGGAATTTTTCGGAATGATCATCTTGCATCATCATTTCTTGGAAATTCGTG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpIleArg 203
DB 553 ATCCAGTATCTTATCGCTTATTTTCAACATGAATATTTATTTGAGCCGTGGAAGCGT 612
QY 204 GluIleLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAATGAGTGCAGAAACCATCTGCACTGACGTCT---GTCTTTCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgIleGlu 243
DB 670 TGTGACACTCATTTACAGAGTACATCTCTCAAGAGATCTCTTCTCAGACAGAA 729
QY 244 ThrThrAlaSerLeuIleSerAspIleSerArgIleValIleSerLeuLeuProSerIle 263
DB 730 GTTCTGCAATCTTTCATTCAGAGACAGAGAGAAAGTATGTCATGTTTCTCTCA 789
QY 264 ArgAlaTyrIleAsnSerAsnValIleAlaSerIleMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGATGACATATGCTTCCAAATGGGCTCTTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgIleValAlaVal 303
DB 850 TGTGTAGCTCTTCCAAAGGGAACATGTTGAATCTGTTAGACCAGAGAAATTAGCCAAAG 909
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Qy 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCystrProTySerLeuThr 323  
Db 910 TCACGGCCATCTCTTACGGGTTTGTGTTGGGCTCCATATCTCTGTACCA 969  
Qy 324 ValIleTySerPhePheProGluArganLeuThrTySerThrTrpTyHisThrAla 343  
Db 970 ATTGCTCTTCAATTTATCTCTCAGCACAGGTCTTAATTCAGTTGTATGAATTGCA 1029  
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyProLeuCyHisIle 363  
Db 1030 TTTTGCTTCACGTGTTCAATCTTTGTCAATCTCTTTGTATCCATGTGTCAAG 1089  
Qy 364 ArgPheGlnTyAlaPheLeuTyIleLeuProValArgArgGlnSerThrPro--Pro 382  
Db 1090 CCCTTTCAAAAGGCTTTTGAATAATTTGTATGAATAAAGCAACCTCACATCACAA 1149  
Qy 383 HisAsnArgSerIleSerThr 389  
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

## RESULT 15

US-10-782-596-13  
Sequence 13, Application US/10782596  
Publication No. US20040137509A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Ruoping  
APPLICANT: Dang, Huang T.  
APPLICANT: Liaw, Chen W.  
APPLICANT: Lin, I-Lin  
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
FILE REFERENCE: AREN0050  
CURRENT APPLICATION NUMBER: US/10782,596  
CURRENT FILING DATE: 2004-02-19  
PRIOR APPLICATION NUMBER: US/09/875,076  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 09/417,044  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: 60/120,416  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 60/121,851  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/123,946  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,949  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/136,436  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,437  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,439  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,567  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-782-596-13

## Alignment Scores:

Pred. No.: 8, 77e-138 Length: 1173  
Score: 1308.50 Matches: 252  
Percent Similarity: 77.52% Conservative: 48  
Best Local Similarity: 65.12% Mismatches: 84  
Query Match: 64.27% Indels: 3  
DB: 19 Gaps: 3

US-10-626-398-10 (1-389) x US-10-782-596-13 (1-1173)

Qy 5 AsnSerThrIleAlaLeuThr--SerIleTySleSerLeuThrPheLeuMetSerLeu 23  
Db 13 AATAGCAACAATCAATTTATCACTAGACACTGCTTACTTATTTGATTTTATGTCCTTA 72  
Qy 24 LeuAlaIleAlaIleMerLeuGlnAsnValValIleLeuAlaPheIleValAspArg 43  
Db 73 GTAGCTTGTGCTATATATCTAGAAATCTTTGGCATTTTATGCTTTGTGTGACAA 132  
Qy 44 AsnLeuArgHisArgSerAsnTySerPhePheLeuAsnLeuAlaIleAlaAspPheVal 63  
Db 133 AACCTTAGACATCAGAGATGATTTTCTTAACTTGGCCATCTGACTCTTTGG 192  
Qy 64 GlnAlaIleAlaIleProLeuTyIleProSerSerLeuThrTyTrpThrSerGly 83  
Db 193 GGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTGAAAGGATTTGAAAG 252  
Qy 84 GlnAlaCyValPheTrpLeuIleThrAspTyLeuLeuCyThrAlaSerValTyAsn 103  
Db 253 GAAATCTGTATTTTGGCTCACTACTATCTGTATGTACAGCATCTGTATATAC 312  
Qy 104 IleValIleuIleSerTyAspArgTyGlnSerValSerAsnAlaValTrpTyArgAla 123  
Db 313 ATTGCTCATCAGCTATGATGATGATCCTGTCAGTCTCAATGCTGTCTTATAGACT 372  
Qy 124 GlnHisSerGlyThrTrpTySleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143  
Db 373 CAACATCTGGGGCTTGAAGATGTACTCTGATGGTGGCCGTTGGGTGCTGGCCTTC 432  
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrArgGly 163  
Db 433 TTAGTGAATGGCCATATATCTAGTTCAGAGCTTGAAGATGAAGTGAATAT 492  
Qy 164 GlnProGlyPheLeuTySerTrpTySerPheAlaLeuProThrSerLeuGlnPheLeu 183  
Db 493 GAACCTGATTTTTTTCGGATGATGATCCTTGCCATCACATCTTGTGAATTCG 552  
Qy 184 IleProIleLeuLeuValAlaTyPheSerAlaHisIleTyTrpSerLeuTrpTySarg 203  
Db 553 ATCCAGCATCTTATGCTTATTTCAATGATATTTATTTGAGCCTGTGGAAGCGT 612  
Qy 204 GlnTySleSerArgCyLeuSerHisProValLeuProSerAspSerSerSerAsp 223  
Db 613 GATCATCTCAGTAGGTGCAAGCCATCTTGACGTGACTGCT--GTCCTTCAACATC 669  
Qy 224 HisGlyHisSerCySargGlnAspProAspSerArgAlaThrLeuProAlaArgTySglu 243  
Db 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTTGTGCATGCAGAGA 729  
Qy 244 ThrThrAlaSerLeuGlySerAspTySerArgTySgluSerSerLeuLeuProSerIle 263  
Db 720 GTTCCTGCATCTTCAATTCAGAGACAGAGAGAGAGAGATGATCTCATGTTTCTCA 789  
Qy 264 ArgAlaTyTrpTyAsnSerAsnValIleAlaSerTySmetGlyPheLeuSerHisSerAsp 283  
Db 790 AGAACCAAGATGAATAGCAATACATTCCTTCAAAAGGGTCTTCTTCCCAATCAGAT 849  
Qy 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGlnLeuPheArgAlaArgTySleuAlaTy 303  
Db 850 TCTGTAGCTCTTCAACCAAGGAACATGTGAATGCTTGAAGCCAGAGATTAACCAAG 909  
Qy 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCystrProTySerLeuThrThr 323  
Db 910 TCACGGCCATCTCTTACGGGTTTGTGTTGGGCTCCATATCTCTGTACCA 969  
Qy 324 ValIleTySerPhePheProGluArganLeuThrTySerThrTrpTyHisThrAla 343  
Db 970 ATTGCTCTTCAATTTATCTCTCAGCAACAGGTCTTAATTCAGTTGTATGAATTGCA 1029  
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyProLeuCyHisIle 363  
Db 1030 TTTTGCTTCACGTGTTCAATCTTTGTCAATCTCTTTGTATCCATGTGTCAAG 1089  
Qy 364 ArgPheGlnTyAlaPheLeuTyIleLeuProValArgArgGlnSerThrPro--Pro 382

Db 1090 CGCTTCAAAAGGCTTCTGAAATATTTGTATATAAAAGCACCTTACCATCACAA 1149  
QY 383 HIAAAnAgSer1LeSerThr 389  
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

Search completed: August 5, 2005, 23:02:00  
Job time : 724 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 01:47:48 ; Search time 40 Seconds  
(without alignments)  
935.708 Million cell updates/sec

Title: US-10-626-398-10  
Perfect score: 2036  
Sequence: 1 MLANNSTALTSIKISLFL.....LKILPVRROSTPEHNRISST 389

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1308.5	64.3	390	2 JC7566	histamine H4 recep
2	414	20.3	639	2 A55019	muscarinic acetyl
3	413.5	20.3	590	2 S47572	muscarinic acetyl
4	410	20.1	486	2 JC1415	histamine H1 recep
5	409.5	20.1	589	2 A29476	muscarinic acetyl
6	407.5	20.0	590	2 S01114	muscarinic acetyl
7	406	19.9	488	2 I56507	histamine H1 recep
8	404.5	19.9	589	2 B29514	muscarinic acetyl
9	403.5	19.8	590	2 S10128	muscarinic acetyl
10	402.5	19.8	531	2 JT0531	muscarinic acetyl
11	392	19.3	466	2 I57959	alpha-1C adrenerg
12	390.5	19.2	460	2 I51837	muscarinic recep
13	390.5	19.2	460	2 A29514	muscarinic acetyl
14	390.5	19.2	532	2 JT0530	muscarinic acetyl
15	389.5	19.1	460	2 S09508	muscarinic acetyl
16	388.5	19.1	460	2 A24325	muscarinic acetyl
17	386.5	19.0	487	2 JC2495	histamine H1 recep
18	385.5	18.9	429	2 S65656	alpha-1C adrenerg
19	385.5	18.9	466	2 JN0765	alpha-1C adrenerg
20	385.5	18.9	499	2 S65657	alpha-1C adrenerg
21	384.5	18.9	466	2 A35375	alpha-1C adrenerg
22	380.5	18.7	491	2 A41632	histamine H1 recep
23	379.5	18.6	490	2 A35546	muscarinic acetyl
24	378	18.6	377	2 A53279	serotonin receptor
25	376.5	18.5	515	2 A40491	alpha-1B adrenerg
26	373.5	18.3	517	2 A45121	alpha-1B adrenerg
27	373	18.3	466	2 S10126	muscarinic acetyl
28	372.5	18.3	460	2 A31897	muscarinic acetyl
29	372	18.3	466	2 A27386	muscarinic acetyl

30	371	18.2	400	2 G00013	D3 dopamine recept
31	371	18.2	466	2 S10856	muscarinic acetyl
32	370	18.2	386	2 S18637	serotonin receptor
33	370	18.2	400	2 G01977	d3 dopamine recept
34	369	18.1	386	2 A42688	serotonin receptor
35	368	18.1	377	2 B30341	G protein-coupled
36	368	18.1	379	2 JC6178	serotonin receptor
37	368	18.1	479	2 S33776	muscarinic acetyl
38	368	18.1	484	2 S58868	G protein-coupled
39	366.5	18.0	515	2 JC1525	alpha-1B adrenerg
40	366	18.0	390	2 JN0268	serotonin receptor
41	365.5	18.0	572	2 I39369	alpha-1A adrenerg
42	364.5	17.9	501	2 JH0447	alpha-1A adrenerg
43	364	17.9	479	2 S10127	muscarinic acetyl
44	363	17.8	466	2 A40972	muscarinic acetyl
45	363	17.8	501	2 T18863	hypothetical prote

## ALIGNMENTS

## RESULT 1

JC7566 histamine H4 receptor, HH4R - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C/Accession: JC7566  
R:Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.  
Biochem. Biophys. Res. Commun. 279, 615-620, 2000  
A:/Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.  
A:/Reference number: JC7566; NCID: 20568725; PMID:11118334  
A:/Contents: Leukocyte  
A:/Accession: JC7566  
A:/Molecule type: mRNA  
A:/Residues: 1-390 <MAX>  
A:/Cross-references: UNIPROT:Q9H3N8; DDBJ:AB045370  
A:/Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled A;Gene: hh4r  
C:/Keywords: G protein-coupled receptor; transmembrane protein

Query Match	64.3%	Score 1308.5;	DB 2;	Length 390;
Best Local Similarity	65.1%;	Pred. No. 1.4e-98;		
Matches 252;	Conservative 48;	Mismatches 84;	Indels 3;	Gaps 3;
QY	5	NSTIALT-SIKSLPTFLMLAIAIMGNVVITLAVDRLNRHRSNTPFLNLAIDFFV	63	
DB	5	NSTINLSLSTRVTLAFMSLVAFAIMGNALVILAFVVDKNLRHRSYFFLNLAIIDFFV	64	
QY	64	GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIYLISYDROVSNAVMYRA	123	
DB	65	GAISIPLYIPHTLFEWDFGKICVFWLITDYLLCTASVYNIYLISYDROVSNAVSRYT	124	
QY	124	CHSGTWKIATOWAVVIFSEFMTNGPMILISDSONSTCEBGFLLKWFALPTSLEFL	183	
DB	125	QHTGVAKITLWVAWVLAFLVNGPMILVSEKMGDSCBCEGFSEWVILATISLEFV	184	
QY	184	IPLLVAIVSAHIYWSLMREKLSRCLSHPVLPSSDSSSDHGHSCQDDPSRATLPARKS	243	
DB	185	IPVILVAIVFNMNIYWSLMREKLSRCLSHPVLPSSDSSSDHGHSCQDDPSRATLPARKS	243	
QY	244	TTASLGSDSRKRSLLPSIRAYKSNVNTASVWGFISHDSLALQOREHILPRARKLAK	303	
DB	244	VPSFHSERQKRKSLMSFSRTRKNSNTASKGSGSOSDSVALHOREHILPRARKLAK	303	
QY	304	SLATLLAFAICWAPYSLTTLVIYSFPERNLTKSTWYTAFWLQWNSFVNPFLYPLCHK	363	
DB	304	SLATLLGVAVCWAPYSLTTLVIYSFYSATGPKSVYRIAFWLQWNSFVNPFLYPLCHK	363	
QY	364	RFQKAFKLKLPVRROSTP-PHNRISST 389		
DB	364	RFQKAFKLKICIKOPLPSOHSRSVSS 390		

RESULT 2  
 A:Residues: 1-590 <LEB>  
 A:Species: Gallus gallus (chicken)  
 C:Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: A55019  
 R:Gadbut, A.P.; Galper, J.B.  
 J. Biol. Chem. 269, 25823-25829, 1994  
 A:Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and  
 A:Reference number: A55019; MUID:9501493; PMID:7923287  
 A:Accession: A55019  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-639 <GAD>  
 A:Cross-references: UNIPROT:P49578; GB:L10617; NID:G530097; PIDN:AAA65961.1; PID:G530098  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: neurotransmitter receptor

Query Match 20.3%; Score 414; DB 2; Length 639;  
 Best Local Similarity 23.4%; Pred. No. 8.9e-26;  
 Matches 125; Conservative 83; Mismatches 145; Indels 182; Gaps 16;

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QY 15 ISLTFLMSLAIATMLGNVVVLAIVDRLRHRSNYEFLNLAIDFVGAIAIPLYIPS 74
DB 117 VLIAFLTGILAVLTIGILVIVSEKVKQKLTNNVYFLSLACADLIIGVISMLFPTY 176
QY 75 SLT--WTSQKQACVFWLITDYLLCTASVYVIVLISYDRYOSVSNVYRAQSGTWKAT 133
DB 177 IIMGMALGNLACDMLSIDYVSNASVNMVLVISPDRYFSITRPLTRAKR--TTKQAG 234
QY 134 QMVAV-WISFPMNGPMILISDSWQNT--STTECEPGLKKWYFALPTSLLEFLIP 185
DB 225 VMIGLAWISFVLWAPALIF--MQYFVGKRTVPDECFIQPLSPITFGTAIAFYLP 291
QY 186 ILVAVPSAHYWSLWK-----RQDPDSR-- 202
DB 292 VTIMSI---LYRRIYKETEKTKELAGLQASGEAETARFVHOTGSSRSLSYELQROS 347
QY 203 -----REKLSRCLSHPVLPSS-----DSSSSDH----- 224
DB 348 TKRSRRKRYRCHFWLTKMSWEPNTDQGDQEHSSDSMNNDAAASLNSASDEEDIT 407
QY 225 -----GHSC-----RQDPDSR-- 241
DB 408 ETRAIYSIVLKLPGHSAILNSTKLPSSEDLNESADELQKSDTDSQKKPKLKQPPKSI 467
QY 242 -----KETTASIGSDSKSRKSSLLPSIRAYKSNVITASMGFLSHSD 283
DB 468 GGSFQKSFSLPIQGSABTATASDGISSVTTSALP--LSFKA--TLAKKFAKTRSQ 524
QY 284 SLALQQRHEILFRARKLAKSLAIIAFAICWAPYSLTTVISFFPERNLTKSTWYHTA 343
DB 525 ---TKRKMSLKEKKAQAQTLSALIFAITWTYNNIMVLVNTCC--DCPKTVNMLG 578
QY 344 FWLQFNFSFVNPFLYPLCHKRFQKAFKLIPV-----RROSTPPHNR 385
DB 579 YVLGYNSTVNPVCYALCNKMFRTFKMLLLCCQDKRRKRKQOYQOROSVIFHKR 633

```

RESULT 3  
 S47572  
 muscarinic acetylcholine receptor m3 - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
 C:Accession: S47572  
 R:Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.  
 Biochim. Biophys. Acta 1223, 151-154, 1994  
 A:Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re  
 A:Reference number: S47572; MUID:94339178; PMID:8061048  
 A:Accession: S47572  
 A:Status: preliminary  
 A:Molecule type: mRNA

A:Residues: 1-590 <LEB>  
 A:Cross-references: UNIPROT:P41984; EMBL:U08286; NID:G520465; PIDN:AAA51866.1; PID:G52046  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: neurotransmitter receptor

Query Match 20.3%; Score 413.5; DB 2; Length 590;  
 Best Local Similarity 24.3%; Pred. No. 8.9e-26;  
 Matches 129; Conservative 80; Mismatches 147; Indels 175; Gaps 17;

```

QY 15 ISLTFLMSLAIATMLGNVVVLAIVDRLRHRSNYEFLNLAIDFVGAIAIPLYIPS 74
DB 69 VPIAFLGVLAIVLTIGILVIVSEKVKQKLTNNVYFLSLACADLIIGVISMLF--- 125
QY 75 SLTY-----WTSQKQACVFWLITDYLLCTASVYVIVLISYDRYOSVSNVYRAQSGTW 129
DB 126 -TTYIIMRMALGNLACDMLSIDYVSNASVNMVLVISPDRYFSITRPLTRAKR--TT 182
QY 130 KIATQMAV-WISFPMNGPMILISDSWQNT--ECEPGLKKWYFALPTSLLEFLI 184
DB 183 KRAGVMIGLAWISFVLWAPALIFWQYFVGKRTVPDECFIQPLSPITFGTAIAFYM 242
QY 185 PILVAVPSAHYWSLWK-----RQDPDSR-- 202
DB 243 PVTIMTI---LYRRIYKETEKTKELAGLQASGEAETARFVHOTGSSRSLSYELQRO 298
QY 203 -----REKLSRCLSHPVLPSSSSDH----- 224
DB 299 SMKRSARKRYRCHFWLTKMSWEPNTDQGDQEHSSDSMNNDAAASLNSASDEEDIG 358
QY 225 -----GHSC-----RQDPDSR--ATLPARKETALSGDK 252
DB 359 SETRAIYSIVLKLPGHSAILNSTKLPSSEDLNESADELQKSDTDSQKKPKLKQPPKSI 418
QY 253 SRRKS-SLTP-----SIRAYKSNV-----IASMGFLSHSDSLAL 287
DB 419 SFQKSFSLPIQLSAVDTAASDVNSVGKTATPLPSFKEATLAKFALKTRSQ--I 475
QY 288 QQRHEILFRARKLAKSLAIIAFAICWAPYSLTTVISFFPERNLTKSTWYHTAFWLQ 347
DB 476 TKRKMSLKEKKAQAQTLSALIFAITWTYNNIMVLVNTCCD--SCIPKTYNMGWILC 533
QY 348 WPNSTFVNPFLYPLCHKRFQKAFKLIPV-----RROSTPPHNR 385
DB 534 YINSTVNPVCYALCNKMFRTFKMLLLCCQDKRRKRKQOYQOROSVIFHKR 584

```

RESULT 4  
 JCI1415  
 histamine H1 receptor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C:Accession: JCI1415  
 R:Fujimoto, K.; Horio, Y.; Sugama, K.; Ito, S.; Liu, Y.Q.; Fukui, H.  
 Biochem. Biophys. Res. Commun. 190, 294-301, 1993  
 A:Title: Genomic cloning of the rat histamine H1 receptor.  
 A:Reference number: JCI1415; MUID:93135784; PMID:7678492  
 A:Accession: JCI1415  
 A:Molecule type: DNA  
 A:Residues: 1-486 <FUJ>  
 A:Cross-references: UNIPROT:P31390; DBJ:D12800; NID:G220770; PIDN:BA02245.1; PID:G22077  
 C:Comment: This Ca2+-mobilizing receptor mediates immune hypersensitivity in peripheral t  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; transmembrane protein  
 F:30-49/Domain: transmembrane #status predicted <TM1>  
 F:64-83/Domain: transmembrane #status predicted <TM2>  
 F:102-121/Domain: transmembrane #status predicted <TM3>  
 F:146-165/Domain: transmembrane #status predicted <TM4>  
 F:190-209/Domain: transmembrane #status predicted <TM5>  
 F:418-437/Domain: transmembrane #status predicted <TM6>  
 F:450-469/Domain: transmembrane #status predicted <TM7>

Query Match 20.1%; Score 410; DB 2; Length 486;  
 Best Local Similarity 24.5%; Pred. No. 1.4e-25;

Matches 118; Conservative 85; Mismatches 163; Indels 116; Gaps 14;

QY 1 MLANNSTILSTIKISLTLFLMSLALAIMGNVVVLAFLVDBNLHRNRYFPLNLAID 60  
DB 14 MCEGNNTAMASPOLLPVLVAVLSISLVATGLNLVLAHSEKRLHTVGLVLSVAD 73  
QY 61 FVGAIAIP---LYIPSSLTWTSGKQACVFWLITVLLCTASVNIIVLISYDRYOSVSN 117  
DB 74 LVGAVVMMNITLYL---ITKMSLGRPLCLFMSMRYASTASIFSVFLICIDRYSVQ 131  
QY 118 AVWYRAQSGTWKIAQWVAWVIFSFMTNGPMILISDSMN-----STTECEBGLK 169  
DB 132 PLRYLYRPTKTRASAT-ILGAMFFSFLMWYPL----GMHFMPPAPBLREDEKCFDFFN 186  
QY 170 KMYFALPJSLLBELILTLVAVYSAHIVMSLMREKLSRCLSPVLPSSD---SSDNG 225  
DB 187 VTMFKIMTAIINFLPTLLMLMFWKIKYAV-RRHCOHQRLTNGSLPSFSELKLRDDTK 245  
QY 226 HSCR-----ODP-----DSRATLP-----ARKETTASLGSDKS 253  
DB 246 EGAKKRGRESPMGVLRPSRDPVGLDQKSTSDPKMTSPTVSOGERTRCRFLDIM 305  
QY 254 RKRSLLPSIRAYKSNVIA-----KMGFLSHSDSLALQO-----289  
DB 306 QKQSVAGDVRGSKANDQALSGPKMDEQSLMTCRRISETSEDTLVDOQSFSRTDSTS 365  
QY 290 -----REH-----IELFARLKLASLALLAFAI 314  
DB 366 IEPGPRVKSRSNGSLDYIKITWRLKLSHRSROYSGHLNERAAQOLGFIAMAFLI 425  
QY 315 CWAPYSLTVIYVFFPERNLTKSTWYHTAFWLMQFNSFVNPFLYPLCHKRFQAFKILP 374  
DB 426 CMIPYIFPMVIAFC--KCCCEPMHMTIWLGINSTLANPLIPLCENPKTKFKILH 483  
QY 375 VR 376  
DB 484 IR 485

RESULT 5

A29476  
muscarinic acetylcholine receptor M4 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #ext\_change 09-Jul-2004  
C/Accession: A29476  
R:Baran, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.  
Biochem. Biophys. Res. Commun. 149, 125-132, 1987  
A>Title: A novel subtype of muscarinic receptor identified by homology screening.  
A:Reference number: A29476; WUID:88077068; PMID:3120722  
A:Accession: A29476  
A:Molecule type: mRNA  
A:Residues: 1-589 <RA>  
A:Cross-references: UNIPROT:P08483; GB:M18088; NID:g202657; PIDN:AAA40659.1; PID:g202658  
A:Experimental source: brain  
C:Superfamily: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane  
C:Keywords: vertebrate rhodopsin  
F:67-90/Domain: transmembrane #status predicted <TM1>  
F:104-124/Domain: transmembrane #status predicted <TM2>  
F:142-163/Domain: transmembrane #status predicted <TM3>  
F:184-206/Domain: transmembrane #status predicted <TM4>  
F:230-251/Domain: transmembrane #status predicted <TM5>  
F:492-512/Domain: transmembrane #status predicted <TM6>  
F:527-545/Domain: transmembrane #status predicted <TM7>

Query Match 20.1%; Score 409.5; DB 2; Length 589;  
Best Local Similarity 24.6%; Pred. No. 1.9e-25;  
Matches 131; Conservative 81; Mismatches 143; Indels 177; Gaps 17;

QY 15 ISLTFLMSLALAIMGNVVVLAFLVDBNLHRNRYFPLNLAIDPFVGAIAIPLYPS 74  
DB 68 VFIAFLTGFLATVITIGNLIVAFVKNQKLTKNVNFLLSLACADLIIGVSMNLF---124  
QY 75 SLTY-----WTSGKQACVFWLITDYLLCTASVNIIVLISYDRYOSVSNVWYRAQSGTW 129

DB 125 -TTYIIMRWALGNLACDLMLSIDVYASNASVNNLVISFDRYFSITRPLTYRAKR--TT 181  
QY 130 KIATQWAV-WIFSPFTNGPMILISDSMNSTT---EEBGLKMYKYPALPSLLEPLI 184  
DB 182 KRAGVMIGLAWISFLMAPAILFMQYFVGKRVPPGECFIOFLSPRTTTFGTAIAAFY 241  
QY 185 PILVAVFAHIVMSLMK-EKLSRCL-----HPLPSSDSSS-----222  
DB 242 PYTIMT---LYRIYKETERKTELQAGSCTAEAEKFNHPTGSSRSCSYELQO 237  
QY 223 -----DHGSCR-----ODPSRATLPARKETTS---247  
DB 298 GYVRSRRRYGRCHFPTTKSMKPSAEQMDQDHSSDSMNNDAAASL-----ENSASSDE 353  
QY 248 --LGSD-----KSRKSLPSIRAYKSNVYASK-----275  
DB 354 EDIGSETRAIYSLVLPQHSSITLNSTKLPSSDNLQVSNEDLGTVDVERNAHLQAKSM 413  
QY 276 -----MGFLSHSDSLA-----286  
DB 414 GGDGNCQKDFTKPIOLBSAVDTGKTSDTNSSADKTTATLPUSFKATLAKRFALTRSQ 473  
QY 287 LQOREHIELEFRKLAISLAILAFAICWAPYSLTVIYVFFPERNLTKSTWYHTAFWL 346  
DB 474 ITRKREMSLIKEMKAQTLASILLAFITWTPYNIWLVNTE--RDSICPKTYMNLGYWL 531  
QY 347 QWNSFVNPFLYPLCHKRFQAFKILPV-----RROSTPPHNR 385  
DB 532 CYNSTVNPVYALCNKTRFTTFKMLLCCQDKRRKROOYQOROSVIFPKR 583

## RESULT 6

S01114  
muscarinic acetylcholine receptor M2, glandular - pig  
N:Alternate names: muscarinic acetylcholine receptor III  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #ext\_change 09-Jul-2004  
C/Accession: S01114  
R:Alida, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.  
FEBS Lett. 235, 257-261, 1988  
A>Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonists  
A:Reference number: S01114; WUID:88296835; PMID:3402600  
A:Accession: S01114  
A:Molecule type: DNA  
A:Residues: 1-590 <AKT>  
A:Cross-references: UNIPROT:P11483; EMBL:X12712; NID:g1861; PIDN:CAA31215.1; PID:g1862  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane  
F:68-91/Domain: transmembrane #status predicted <TM1>  
F:105-125/Domain: transmembrane #status predicted <TM2>  
F:143-164/Domain: transmembrane #status predicted <TM3>  
F:185-207/Domain: transmembrane #status predicted <TM4>  
F:231-252/Domain: transmembrane #status predicted <TM5>  
F:493-513/Domain: transmembrane #status predicted <TM6>  
F:528-546/Domain: transmembrane #status predicted <TM7>

Query Match 20.0%; Score 407.5; DB 2; Length 590;  
Best Local Similarity 24.1%; Pred. No. 2.7e-25;  
Matches 129; Conservative 83; Mismatches 140; Indels 183; Gaps 17;

QY 15 ISLTFLMSLALAIMGNVVVLAFLVDBNLHRNRYFPLNLAIDPFVGAIAIPLYPS 74  
DB 69 VFIAFLTGFLATVITIGNLIVAFVKNQKLTKNVNFLLSLACADLIIGVSMNLF---125  
QY 75 SLTY-----WTSGKQACVFWLITDYLLCTASVNIIVLISYDRYOSVSNVWYRAQSGTW 129  
DB 126 -TTYIIMRWALGNLACDLMLSIDVYASNASVNNLVISFDRYFSITRPLTYRAKR--TT 182  
QY 130 KIATQWAV-WIFSPFTNGPMILISDSMNSTT---EEBGLKMYKYPALPSLLEPLI 184  
DB 183 KRAGVMIGLAWISFLMAPAILFMQYFVGKRVPPGECFIOFLSPRTTTFGTAIAAFY 242



QY 15 ISLTFLMSLAIAMIGNVVILAFIVDRNLRRSNVFFNLAIADPFVGAIAPIPIPS 74  
D 68 VFIAFLTGFLATVITIGNIIVIAFKVNNKQTKVNNYFLLSLACADLIIVISIMNF--- 124  
QY 75 SLTY-----WTSKQACVFWLITDYLCTASVYNIIVLISYDRYQSVSNVAVRAQSGTW 129  
D 125 -TTYIIMNRWALGNLACDLWLSIDYVANSVNNLVISFDRYFSITRPLTYBAKRT-TK 182  
QY 130 KATQVAVVWIFSPMNGMILISDSWQNST---ECEGFLKKWYFALPTSLLEFLP 185  
D 183 RGVWIGLAWVLSFVMAPIFLWQYFVGKRTVPGECFIQFLSEPTTFGTIAIAFYMP 242  
QY 186 ILLVAFSAHIYWSLWK-EKLSRCL-----HPVLPSDSSS----- 222  
D 243 VITMTI-----LYRIYKETEKRTKELAGLQASGTEAEAFVPTGSSRSCSYELQQG 298  
QY 223 -----DHGSCR---ODPSRATLPARKETTA--- 247  
D 299 VKRSSRRKYGRCHFMTTKSWKPSAQMDQDHSSSDSMNNDAASL---ENSASDEE 354  
QY 248 -IGSD-----KRRKSLPSIRAYKSNVIAK----- 275  
D 355 DIGSETRAIYSIVLKLPGHSSILNSTKLPSSDNLQVSNEDLGTVDVERNAHKLQAKSMG 414  
QY 276 -----MGFLSHSDSLA-----L 287  
D 415 DGNQCKQDFTKLPQLQESAVDTGKTSNTSSADKTATLPLSFKEATLAKRFLKTRSQI 474  
QY 288 QOREHIELFRARKLAKSLAILLAFAICWAPYSLTTVIYSFFPERNLTKSTWYHTAFTW 347  
D 475 TKRKMSLJKEKKAQTLISAIIAFLITWTVPYNIWLVNTPCD--SCIPKTVNWLGVWLC 532  
QY 348 WENSPFNPLFLYPLCHKRFQKAFILKLPV-----RROSTPPHNR 385  
D 533 YINSTVNPVCYALCNKTFRTFTLLCCQDKRRKQYQOQSVIFPKR 583

## RESULT 9

S10128  
muscarinic acetylcholine receptor M4 - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C/Accession: S10128  
R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A/Title: Distinct primary structures, ligand-binding properties and tissue-specific exp  
A/Reference number: S04326; WUID:8816632; PMID:3443095  
A/Accession: S10128  
A/Molecule type: DNA  
A/Residues: 1-590 <PER>  
A/Cross-references: UNIPROT:P20309; EMBL:X15266; NID:932323; PIDN:CAJ3337.1; PID:932324  
C/Superfamily: Vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme  
F:68-95/Domain: transmembrane #status predicted <TM1>  
F:105-131/Domain: transmembrane #status predicted <TM2>  
F:143-164/Domain: transmembrane #status predicted <TM3>  
F:185-207/Domain: transmembrane #status predicted <TM4>  
F:231-252/Domain: transmembrane #status predicted <TM5>  
F:293-313/Domain: transmembrane #status predicted <TM6>  
F:325-346/Domain: transmembrane #status predicted <TM7>  
F:525-546/Domain: transmembrane #status predicted <TM7>  
F:5,6,15,41/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 19.8%; Score 403.5; DB 2; Length 590;  
Best Local Similarity 23.1%; Pred. No. 5,8e-25;  
Matches 124; Conservative 83; Mismatches 146; Indels 183; Gaps 16;  
QY 15 ISLTFLMSLAIAMIGNVVILAFIVDRNLRRSNVFFNLAIADPFVGAIAPIPIPS 74  
D 68 VFIAFLTGFLATVITIGNIIVIAFKVNNKQTKVNNYFLLSLACADLIIVISIMNF--- 125  
QY 75 SLTY-----WTSKQACVFWLITDYLCTASVYNIIVLISYDRYQSVSNVAVRAQSGTW 129  
D 125 -TTYIIMNRWALGNLACDLWLSIDYVANSVNNLVISFDRYFSITRPLTYBAKRT-TT 182

QY 130 KATQVAVVWIFSPMNGMILISDSWQNST---ECEGFLKKWYFALPTSLLEFLP 184  
D 183 RGVWIGLAWVLSFVMAPIFLWQYFVGKRTVPGECFIQFLSEPTTFGTIAIAFYM 242  
QY 185 ILLVAFSAHIYWSLWK-----LSHPVLPSDSSSDH----- 202  
D 243 VITMTI-----LYRIYKETEKRTKELAGLQASGTEAEAFVPTGSSRSCSYELQQG 298  
QY 203 -----REKLSRC----- 224  
D 299 VKRSSRRKYGRCHFMTTKSWKPSAQMDQDHSSSDSMNNDAASL---ENSASDEE 358  
QY 225 -----GHSC----- 231  
D 359 SEETRAIYSIVLKLPGHSSILNSTKLPSSDNLQVPEBELGVDERKADKLQAKSYDDG 418  
QY 232 --PDSRATLPARKET-----TASLGSDRKRRKSLPSIRAYKSNVIAKMGFLSHD 283  
D 419 SFPKSPSKLPQLQESAVDTGKTSNTSSADKTATLPLSFKEATLAKRFLKTRSQI 474  
QY 284 SLAQOREHIELFRARKLAKSLAILLAFAICWAPYSLTTVIYSFFPERNLTKSTWYHTA 343  
D 475 -ITRKMSLJKEKKAQTLISAIIAFLITWTVPYNIWLVNTPCD--SCIPKTFWNLG 529  
QY 344 FWLQWNSFVNPLFLYPLCHKRFQKAFILKLPV-----RROSTPPHNR 386  
D 530 YWLCYNSTVNPVCYALCNKTFRTFTLLCCQDKRRKQYQOQSVIFPKRA 585

## RESULT 10

JT0531  
muscarinic acetylcholine receptor M5 - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C/Accession: JT0531; A33354; C37121  
R:Boerner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.  
Neuron 1, 403-410, 1988  
A/Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor  
A/Reference number: JT0530; WUID:9016521; PMID:3272174  
A/Accession: JT0531  
A/Molecule type: DNA  
A/Residues: 1-531 <BON>  
A/Cross-references: UNIPROT:P08911  
R:Uiao, C.F.; Thiemmen, A.P.N.; Joho, R.; Barberis, C.; Birnbaumer, M.; Birnbaumer, L.  
J. Biol. Chem. 264, 7328-7337, 1989  
A/Title: Molecular cloning and expression of a fifth muscarinic acetylcholine receptor.  
A/Reference number: A33354; WUID:89214170; PMID:2540186  
A/Accession: A33354  
A/Molecule type: DNA  
A/Residues: 1-531 <LIA>  
A/Cross-references: GB:M2925; NID:920511; PIDN:AAA4157.1; PID:9205312; GB:J04706  
C/Superfamily: Vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
F:29-52/Domain: transmembrane #status predicted <TM1>  
F:66-86/Domain: transmembrane #status predicted <TM2>  
F:104-125/Domain: transmembrane #status predicted <TM3>  
F:146-168/Domain: transmembrane #status predicted <TM4>  
F:191-213/Domain: transmembrane #status predicted <TM5>  
F:243-263/Domain: transmembrane #status predicted <TM6>  
F:288-308/Domain: transmembrane #status predicted <TM7>  
F:478-496/Domain: transmembrane #status predicted <TM7>  
F:7,12/Binding site: carbohydrate (Aan) (covalent) #status predicted



```

Db      94  GTLACDLALADYVANSNAYNNLLISFDRIYTSVTRPLSYRAK--TPRRALMILAND 151
QY      141  FSPMTNGEMILISDSWONSTTE-----CEBGFLKMYFALPTSLLEPLILVAYES 193
Db      152  VSFVLMAPALIF---NQYLGBERTVLAGCYIQLFSLQPIITFGTAMAAFYLPVPTVM---- 204
QY      194  AHYWSLKKRELTSRCLSHPLVR-----SDSSSHS-----GHSGR-- 229
Db      205  CTLVWRIY-RETENPARELALAQSETPCKGGGSSSSSSSSERSOPGAEGPSPEPRGRCRCC 263
QY      230  -----OPDSRATLPARKETASLGSDDRKSSSL 259
Db      264  RAPRLQAYSMKEEBEDBGSMESLTSRGEPRGSVVIKMWDBEAOPTKOPKSPS 323
QY      260  LPSIRAYNNSNVIASKMGFLSHSDSLAQOREHIELFRARLAKSLAIIILAAFAICWADY 319
Db      324  NTVVKPTKKGRDGGCKGKPRGKEOLA--KRTPTSLVKEKKAAARTSAIIILAFILTWTPY 381
QY      320  SLTTIVISFFPRERNLTKSTWYHTAFLQWFNSEFVNPFLYRLHCKRQKQAFILTPVR 376
Db      382  NIMVLVSTFC--KDCVPEPTLELQWLCVNSVTVMCMALCNKARDFRILLRCL 436

```

## RESULT 13

muscarinic acetylcholine receptor M1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: A94518; A94293; A37121; A29514  
R:Bonner, T.I.  
submitted to GenBank, July 1987  
A:Reference number: A94518  
A:Accession: A94518  
A:Molecule type: mRNA  
A:Residues: 1-460 <BO1>  
A:Cross-references: UNIPROT:P08482  
R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.  
Science 237, 527-532, 1987  
A:Title: Identification of a family of muscarinic acetylcholine receptor genes.  
A:Reference number: A94293; MUID:87263421; PMID:3037705  
A:Accession: A94293  
A:Molecule type: mRNA  
A:Residues: 1-227;338-460 <BO2>  
A:Experimental source: cerebral cortex  
A:Note: only a part of the protein translation is given; none of the nucleotide sequence  
R:Kartenbach, E.; Curtis, C.A.M.; Pедder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.  
J. Biol. Chem. 265, 13702-13708, 1990  
A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv  
A:Reference number: A37121; MUID:90337982; PMID:2380182  
A:Accession: A37121  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 62-124 <KUR>  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
E:25-50/Domain: transmembrane #status predicted <TM1>  
E:62-93/Domain: transmembrane #status predicted <TM2>  
E:100-121/Domain: transmembrane #status predicted <TM3>  
E:142-168/Domain: transmembrane #status predicted <TM4>  
E:187-209/Domain: transmembrane #status predicted <TM5>  
E:367-387/Domain: transmembrane #status predicted <TM6>  
E:402-420/Domain: transmembrane #status predicted <TM7>  
E:12/Binding site: carbohydrate (Asn) (covalent) #status predicted

	Query Match	19.2%	Score 390.5	DB 2:	Length 460:
	Best Local Similarity	27.3%	Pred. No. 4,9e-24:		
	Matches 114:	Conservative 68:	Mismatches 150:	Indels 77:	Gaps 12:
Qy	23	LLAATMGGVVVLTATVYDNRLLRHSRVSFLNTAIDPFGAIAPIYISSLT-VYTS	81		
Db	34	LSLATVGNGLIVLSPKRVNTELRKVVNYFLSLACADIIIGTSPMNLVTTLLMGHVAL	93		

[illegible]

## RESULT 14

muscarinic acetylcholine receptor M5 - human  
C.Species: Homo sapiens (man)  
C.Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #ext\_change 21-Jan-2000  
C.Accession: J10530  
R.Bonner, T. I.; Young, A. C.; Brann, M. R.; Buckley, N. J.  
Neuron 1, 403-410, 1988  
A.Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor  
A.Reference number: J10530; MUID:90166521; PMID:3272174  
A.Accession: J10530  
A.Molecule type: DNA  
A.Residues: 1-532 <BON>  
C.Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotransmitter acetylcholine.  
C.Superfamily: vertebrate rhodopsin  
C.Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipid binding site  
F.30-53/Domain: transmembrane #status predicted <TM1>  
F.67-87/Domain: transmembrane #status predicted <TM2>  
F.105-126/Domain: transmembrane #status predicted <TM3>  
F.147-169/Domain: transmembrane #status predicted <TM4>  
F.192-211/Domain: transmembrane #status predicted <TM5>  
F.444-466/Domain: transmembrane #status predicted <TM6>  
F.479-498/Domain: transmembrane #status predicted <TM7>  
F.8-13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query	March	19.2%	Score	390.5	DB	2	Length	533	
Best Local	Similarity	24.2%	Pred.	5.8e-24					
Matches	121	Conservative	78	Mismatches	146	Indels	155	Gaps	16
Qy	15	ISLFLMSLLAIATMLGNVVVILAFVDRNLRRHSNYFFLNLAIDFVGAIAIPLYPS	74						
Db	31	ITIAAVTAIVSVLLITVGNVLVMIISFKVNSQKLTNYNYLLIACADLLSGIFSNMLY---	87						
Qy	75	SLTV-----WTSGQACVCFMLITDYLCTASVYVIVLISYDRYOSVSNAAVYRAQHGSTM	129						
Db	68	-TYYILMRMALGSLACDMLALDIYVSNASVNMVLIVISPRYSITPLEYTRAGR--TP	144						
Qy	130	KIATQMAV-VIFSEMTNGEMILISDSWQ-----STECGEGFLKMWYALFTSLLE	181						
Db	145	KRAGIMIGLAWLISFILMAPAIL---CMQYLVGRKRVPLDCQIOFLSEPTITFGTAIAA	201						
Qy	182	FLIPILLVAVPSAIIY-----	197						
Db	202	FYIFVSVWTLIYCHYIRETEKRTDLDLQSSDSVTYAKERRKPAHRALFRSCIRCPRTL	261						
Qy	198	-----WGL-----W-KREGLSACLSHPVLPSDSSSDHGHS	227						
Db	262	AQRRNQASWSSSRSTTTGKPSQATGSPANMAKAEGLLTCCSSYP-----SSDEDKQ	315						

QY 228 C-----KODPSRATLPARKETTASLGSDKS--RRKSLLPSIRAY--KNSN 270  
DB 316 ATDPVLQVYVYKSGKESPEEFESABETETFPVKATREKSDVDTPTVLLSPAANRPKGX 375  
QY 271 VIASMGFLSHSD-----SLAQOREHIELF 296  
DB 376 CVAYKFRVLVVKADGQOETNNGCHKVKIMPCPPVAKPEPTKGLNPNPSHQTKRKRVVLV 435  
QY 297 RARKLAKSLAILLAAFAICWAPYSLTIVYSFPERNLKSTWYHTAFWLQMFNSPVNPF 356  
DB 436 KERKAQUTLSAILLAFILITWTPYNI-MVLVSTFCDCVCVFTLM-HLGWLCYVNSTVNI 493  
QY 357 LYPILCKRFOKAFELKILPVR 376  
DB 494 CYALCNRTFRKTFKMLLCLR 513

## RESULT 15

S09508  
muscarinic acetylcholine receptor M1 - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text\_change 03-Jul-2004  
C/Accession: S09508; S06327; S04326  
R/Chapman, C.G.; Browne, M.J.  
Nucleic Acids Res. 18, 2191, 1990  
A/Title: Isolation of the human m1 (Hm1) muscarinic acetylcholine receptor gene by PCR a  
A/Reference number: S09508; MUID:90245564; PMID:3336407  
A/Accession: S09508  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-460 <CHA>  
A/Cross-references: UNIPROT:P11229; EMBL:X52068; NID:G34450; PIDN:CAA36291.1; PID:G34451  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990  
R/Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.  
Nucleic Acids Res. 15, 10604, 1987  
A/Title: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.  
A/Reference number: S06327; MUID:88096607; PMID:3697105  
A/Accession: S06327  
A/Molecule type: DNA  
A/Residues: 1-460 <ALL>  
A/Cross-references: GB:Y00508; GB:M5128; NID:G297405; PIDN:CAA68560.1; PID:G297406  
R/Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A/Title: Distinct primary structures, ligand-binding properties and tissue-specific expr  
A/Reference number: S04326; MUID:88166632; PMID:3443095  
A/Accession: S04326  
A/Molecule type: DNA  
A/Residues: 1-172, 'M', 174-460 <PER>  
A/Cross-references: EMBL:X15263; NID:G32317; PIDN:CAA33334.1; PID:G32318  
A/Superfamily: Vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
P:25-50/Domain: transmembrane #status predicted <TM1>  
P:62-93/Domain: transmembrane #status predicted <TM2>  
P:100-121/Domain: transmembrane #status predicted <TM3>  
P:142-168/Domain: transmembrane #status predicted <TM4>  
P:187-209/Domain: transmembrane #status predicted <TM5>  
P:367-387/Domain: transmembrane #status predicted <TM6>  
P:402-420/Domain: transmembrane #status predicted <TM7>  
P:2,12/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 19.1%; Score 389.5; DB 2; length 460;  
Best Local Similarity 27.1%; Pred. No. 5.9e-24;  
Matches 115; Conservative 72; Mismatches 145; Indels 93; Gaps 15;

QY 23 LLAIMIGNVVYIAFYDRNLHRNSYFFLNLAIADFFGALAIPLYIPSSLT-YWTS 81  
DB 34 LLSLATVIGNLVLISFKVNTLKTNNYFLSLACADLIIGTFSMNLVYTLILMGHWAL 93  
QY 82 GKQACVFMILITDYLCSTSVNIVIVISYRQSVSNAAVYRAOHSGTWKIATQWAV-WI 140  
DB 94 GTLACDMLIALDYSVSNASVNNLLISFDRYFSVTRPLSYRAKR--TPRRALMIGLAWL 151

QY 141 FSPMTNGFMILISDSWONSTTE-----CEPFLKKVYFALPTSLLEFLIPILLVAYFS 193  
DB 152 VSFVLMAPIILF---WQYLGERTVLAGQCYIQFLSQPIITFGTMAAFILPVTVM----- 204  
QY 194 AHYWSLMKREKLRCLSHPLVP-----SDSSSDH-----GHSCR-- 229  
DB 205 CTLVWRIY-RETEENRARELALQGETPGKGGSSSSSERGQPGAEGSPETPPGRCCRC 263  
QY 230 -----ODPSRATLPARKETTASLGSDKSRRKSLPSI----- 263  
DB 264 RAPRLQAYSMKEEEDSGMESL-----TSSEGEPSGVIVIKMPVDEAQAPTKQ 317  
QY 264 --RAYKSNVIASIKXGFLSHSDSLA-----LQOREHIELFRARLAKSLAILLAA 311  
DB 318 PPRSSPNTVKRPTKKG---RBRAGKQKPRGKEQLAKRTFSLVKEKKAARTLSAILLA 373  
QY 312 FAICWAPYSLTIVYSFPERNLKSTWYHTAFWLQMFNSPVNPFILPILCHRFQKAPLK 371  
DB 374 FILWTPYNIWLVSTFC--KDCVPELIMELGYWLCYVNSTINPCVYALCNKAFRDTFRL 431  
QY 372 ILPVR 376  
DB 432 LLLCR 436

Search completed: August 3, 2005, 01:57:48  
Job time : 43 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OW protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 20:15:21 ; Search time 3171 Seconds  
(without alignments)  
4669.505 Million cell updates/sec

Title: US-10-626-398-10  
Perfect score: 2036  
Sequence: 1 MLANNSTALTSIKISLFTL.....LKILPVROSTPPHNSIST 389

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgr2\_1/USPTO.epool\_p/US10626398/runat\_02082005.155808.2927/app\_query.fasta.1.583  
-DB=EST -QPM=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPEXT=0 -LIST=45  
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-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTPM=pro -NORP=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10626398.qcgn\_1.1.5180@runat.02082005.155808.2927 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:.\*  
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2: gb\_est2:.\*  
3: gb\_hic:.\*  
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6: gb\_est5:.\*  
7: gb\_est6:.\*  
8: gb\_ges1:.\*  
9: gb\_ges2:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	817	40.1	839	5	BX643713 DKFZp781C
2	806.5	39.6	704	7	CF147821 AGENCOURT
3	460	22.6	732	7	CF147822 AGENCOURT
4	443.5	21.8	721	7	CO959034 AGENCOURT
5	404.5	19.9	1770	9	AY400784 Mus muscu
6	404.5	19.9	3171	3	AK080950 Mus muscu
7	403.5	19.8	1773	9	AY400782 Homo sapi
8	402	19.7	2760	3	AK032763 Mus muscu
9	402	19.7	2831	3	AK047070 Mus muscu

10	402	19.7	2979	3	AK038480
11	402	19.7	3783	3	AK046607 Mus muscu
12	394.5	19.4	853	6	CD326085 AGENCOURT
13	391.5	19.2	672	6	CB556920 CB556920 AKGNINC:U
14	391	19.2	1401	9	AY39428 Mus muscu
15	391	19.2	4124	3	AK085653 Mus muscu
16	389.5	19.1	4135	3	AK079597 Mus muscu
17	388.5	19.1	3816	3	AK081248 Mus muscu
18	384	18.9	1401	9	AY399426 Homo sapi
19	378	18.6	1134	9	AY188218 Homo sapi
20	376.5	18.5	1764	3	BC018330 Mus muscu
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22	376.5	18.5	3050	3	AK03877 Mus muscu
23	370	18.2	1203	9	AY407499 Homo sapi
24	369	18.1	1161	9	AY415607 Mus muscu
25	368	18.1	1203	9	AY407500 Pan trogl
26	368	18.1	1440	9	AY404936 Mus muscu
27	366	18.0	1173	9	AY415605 Homo sapi
28	366	18.0	1440	9	AY404935 Pan trogl
29	364	17.9	1440	9	AY404934 Homo sapi
30	364	17.7	1125	9	AY418220 Mus muscu
31	361	17.7	1173	9	AY415606 Pan trogl
32	361	17.7	2908	3	AK082016 Mus muscu
33	356.5	17.5	1200	9	AY407501 Mus muscu
34	356	17.5	2232	3	CR606112 full-length
35	352.5	17.3	1072	9	AY398880 Homo sapi
36	348	17.1	1332	9	AY418851 Homo sapi
37	347	17.0	1347	9	AY416858 Mus muscu
38	347	17.0	2578	3	AK045364 Mus muscu
39	345.5	17.0	1072	9	AY398881 Pan trogl
40	342.5	16.8	1335	9	AY418853 Mus muscu
41	336.5	16.5	716	7	CN423054 AY398882
42	335.5	16.5	1069	2	AY398882
43	328.5	16.1	499	2	BF567596 UI-R-B00
44	328	16.1	1167	9	AY416975 Mus muscu
45	327	16.1	1141	9	AY416974 Pan trogl

#### ALIGNMENTS

RESULT 1  
BX643713  
LOCUS  
DEFINITION BX643713 839 bp mRNA linear EST 04-SEP-2003  
ACCESSION DKFZp781C0629.5, mRNA sequence.  
VERSION BX643713 GI:34478046  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Homo sapiens

REFERENCE  
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 839)  
Rober, G., Han, M., Bahr, A., Mewes, H.W., Weil, B., Amlid, C., Osanger, A.,  
EST (Lauder, J., Bahr, A., Mewes, H.W., Weil, B., Amlid, C., et al.)  
Unpublished (2003)  
Contact: MIPS

TITLE  
JOURNAL  
COMMENT  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden, Germany) within the CDNA sequencing  
consortium of the German Genome Project.  
No 5' sequence available.  
This clone (DKFZp781C0629) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcentzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
source  
1..839  
/organism="Homo sapiens"  
/mol\_type="mRNA"

/db\_xref="taxon:9606"  
 /clone="DKFZP781C0629"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_1lb="781 (synonym: hlc64)"  
 /note="Vector: pSPORT1\_Sfi; Site\_1: SfiIA; Site\_2: SfiIB;  
 cDNA-collection"

# ORIGIN

## Alignment Scores:

Pred. No.:	1,846-73	Length:	839
Score:	817.00	Matches:	160
Percent Similarity:	78.69%	Conservative:	32
Best Local Similarity:	65.57%	Mismatches:	50
Query Match:	40.13%	Indels:	3
DB:	5	Gaps:	2

US-10-626-398-10 (1-389) x BK643713 (1-839)

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QY 5 AanserThrIleAlaLeuThr---SerIleYsIleSerLeuThrPheLeuMetSerLeu 23
DB 108 AATAGACAAATCAATTTATTCACAGACCTCGGTACTTTCAGATTTCATTTATGTCCTTA 167
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 168 GTAGCTTTGCTATATGCTAGAAATGCTTGCTATTTAGCTTTGCTGTCGACAA 227
QY 44 AenLeuArgHisArgSerAsnTyrrPheLeuAsnLeuAlaIleAlaAspPheVal 63
DB 228 AACCTTAGACATCGAAGTATGTTATTTTCTTAACCTTGCCATCTGACCTTCCTTGG 287
QY 64 GAlaAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrPheSerGlyLys 83
DB 288 GGTGTGATCTCATCTTCTTGTACATCCTCACAGCCTTTCGAAATGGATTTGGAAAG 347
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrrLeuLeuCysThrAlaSerValTyra 103
DB 348 GAAACTGTGTATTTGGCTCACTGACTGACTGCTGTTGTATGACAGCATCTGTATATAAC 407
QY 104 ILeValIleIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaValTrpTyrrArgAla 123
DB 408 ATTGCTCATATGCTATATGATGATCCGTGACGTGCTCAAAAGCTGTGTCTTATAGAACT 467
QY 124 GlnHisSerGlyThrTrpValIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 468 CAACACTACGGGGTCTGAAGATTGTTACTCGATGCTGGCGTTGGTGGCGGCTTC 527
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGluCys 163
DB 528 TTAGTGAATGGGCAATGATTTCTAGATTTCAGAGTCTTGAGAGAGATGAAGTGTGATGT 587
QY 164 GluProGlyPheLeuLysTrpTyrrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
DB 588 GAACCTGGATTTTTCGAAATGATGATCCTTGCCATCATCATCTTTCGAAATTCGG 647
QY 184 ILeProIleLeuLeuValAlaTyrrPheSerAlaHisIleTyrrPheSerLeuTrpLysArg 203
DB 648 ATCCGACGATCTTACTGCTTATTTTCAACATGAATATTTATTTGAGCGCTGGAAAGCCT 707
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 708 GATCATCTAGTAGAGGCAAGCCATCTGACACTGCTGTCTCTTCCACATCTGT- 766
QY 224 HLeGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaTrpGlyGlu 243
DB 767 ---GGACATCTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTTTCGATCGACAGAA 823
QY 244 ThrThrAlaSer 247
DB 824 GTTCCGATCC 835

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RESULT 2  
 ,CF147821

LOCUS CF147821 704 bp mRNA linear EST 25-JUL-2003  
 DEFINITION AGENCOURT 14740195 NIH MGC 145 Homo sapiens cDNA clone  
 IMAGE:6971900 5', mRNA sequence.  
 ACCESSION CF147821  
 VERSION CF147821.1 GI:33244089  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 704)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: GPCR Consortium  
 cDNA Library Preparation: GPCR Consortium  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: IRB102 row: b column: 07  
 High quality sequence atop: 685.  
 Location/Qualifiers  
 1..704

## FEATURES

source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6971900"  
 /issue\_type="mixed"  
 /lab\_host="DH10B"  
 /clone\_1lb="NIH\_MGC\_145"  
 /note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmiI/XhoI-3', 5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearrayed\\_plates/IRB1.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat)  
 a Note: this is a NIH\_MGC Library."

## ORIGIN

### Alignment Scores:

Pred. No.:	1,696-72	Length:	704
Score:	806.50	Matches:	151
Percent Similarity:	81.25%	Conservative:	31
Best Local Similarity:	67.41%	Mismatches:	41
Query Match:	39.61%	Indels:	1
DB:	7	Gaps:	1

US-10-626-398-10 (1-389) x CF147821 (1-704)

```

QY 5 AanserThrIleAlaLeuThr---SerIleYsIleSerLeuThrPheLeuMetSerLeu 23
DB 11 AATACACAAATCAATTTATTCACAGACCTCGGTACTTTCAGATTTCATTTATGTCCTTA 70
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 71 GTAGCTTTGCTATATGCTAGAAATGCTTGTCATTTAGCTTTTCGTGTCGACAA 130
QY 44 AenLeuArgHisArgSerAsnTyrrPheLeuAsnLeuAlaIleAlaAspPheVal 63
DB 131 AACCTTAGACATCGAAGTATGTTTCTTAACCTTGCCATCTGACCTTCCTTGG 190
QY 64 GAlaAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrPheSerGlyLys 83
DB 191 GGTGTGATCTCATCTTCTTGTACATCCTCACAGCCTGTCGAAATGGATTTGGAAAG 250

```



## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 721)  
NIH-MGC http://mgc.ncl.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
National Cancer Institute / NIH  
Bldg. 31 Rm10N07 Bethesda, MD 20892  
Email: cgsabbs-r@mail.nih.gov  
Tissue Procurement: Guthrie cDNA Resource Center  
cDNA Library Preparation: Guthrie cDNA Resource Center  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRB18 row: a column: 04  
High quality sequence start: 2  
High quality sequence stop: 328.  
Location/Qualifiers

## FEATURES

1..721  
/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:7389774"

/tissue\_type="mixed"

/lab\_host="DH10B (T1-phage-resistant)"

/clone\_lib="NIH-MGC\_146"

/note="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file ftp://image.llnl.gov/image.rearrayed\_plates/IRBF.presv.dat a. Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 5,96e-35 Length: 721  
Score: 443.50 Matches: 87  
Percent Similarity: 80.77% Conservative: 18  
Best Local Similarity: 66.92% Mismatches: 24  
Query Match: 21.78% Indels: 1  
DB: 7 Gaps: 1

US-10-626-398-10 (1-389) x CO959034 (1-721)

QY 5 AensertThlleleuThr---SerlelySleSerleuThrPhelueMetSerleu 23  
DB 34 AATAGACATCAATTAATCACTAGACACTCGATTGATCTTTTATATGCTTA 93  
QY 24 leualailealailemetleuglyanvalaileleualaipheilevalaspar 43  
DB 94 GTAGCTTTGCTATATAGTAGGAATGCTTTGCTATTTAGCTTTGTGACAA 153  
QY 44 AenleuAghiaArgSerAntyRphepheleuAenleualailealaSphpheval 63  
DB 154 AACCTTAGACATGGAAGTAGTATTTTCTTAACCTTGCCATCTGACATCTTTG 213  
QY 64 GYAAlailealaileProleuTyRleProSerSerleuThyTyRPhrSerGlyys 83  
DB 214 GGTGGATCTCCATTCCTTTGATACATCCCTCACAGCGCTTGCAGATGGATTTG 273  
QY 84 GlnalaCyvalaPhetRpeleuileThraSPYTyRleuCyethraIaseValTyraen 103  
DB 274 GAATCTGTGATTTTGGCTCACTGACTATCTGTTATGTACCGACATGATATAG 333  
QY 104 llevalleuileSerTyRasparGTYRginSerValSerAsnalaValTrpTyRgala 123

|||||  
334 ATTGCCCTCAGCTATGATAAATCAATCTGATCAATGCTTTATGAAACG 393

QY 124 GlnHisSerGlyThrTrpylelleleuThr 133  
DB 394 CAAAAACGGGGGCGCTGAAGAGGGGAACG 423

## RESULT 5

AY400784

LOCUS

DEFINITION

GENOMIC SURVEY SEQUENCE.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 1770)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,

Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,

Adams,M.D. and Cargill,M.

Interring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 1770)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,

Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.O.,

Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

1..1770

/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

<1..>1770

/gene="CHRM3"

/locus\_tag="HGM0672"

## Alignment Scores:

Pred. No.: 2,71e-30 Length: 1770  
Score: 404.50 Matches: 131  
Percent Similarity: 40.00% Conservative: 83  
Best Local Similarity: 24.49% Mismatches: 138  
Query Match: 19.87% Indels: 183  
DB: 9 Gaps: 19

US-10-626-398-10 (1-389) x AY400784 (1-1770)

QY 15 lIeSerleuThrPhleuMetSerleuAilaileleuGllyanvalaVal 34  
DB 202 GCTTCATTCATTCATTCATTCGCTTCCTGCGATTCGATTCGCAACATCCCTT 261  
QY 35 ValIleleualaipheilevalasparGAsnleuAghiaArgSerAntyRphepheleu 54  
DB 262 GTCATTCGCGATTTAAGTCAACAACAGCAGTGAAGACGTAACACTTCCTCTTA 321  
QY 55 AenleualailealaSphphephevalaIglalailealaileProleuTyRleProser 74  
DB 322 AGCTGCGCTGCGCAGATCTGATCATCGGGGCTTCATTCATGAACTGCTTC 372  
QY 75 SerleuThyTyR-----ThrPhrSerGlyysGlnalaCyvalaPhetR 89  
DB 373 --ACGACCTACATCATTAATGAACCGCTGCGCTCGGGAACCTTAGCCTCTGG 429

QY	90	neulIethrAprrleuLeuCyethrAlaserValTyrAsnIleValleuIleSerTyr	109
Db	430	CTTTCATGTGCTAATGTGGCCAGCAATCTCTCTGTGATCAATATCGCTGGTATGACGTTT	489
QY	110	AspArGTyrGlnSerValSerAsnAlaValTrpTyrArgAlaGlnHisSerGlyThrTrp	129
Db	490	GACAGTACTTTCTTATTAACAGGCCACTCTTACCGAGCCAAAGCA-----ACAACA	543
QY	130	LysIleAlaThrGlnMetValAlaVal---TrpIlePheSerPheMetThrAsnGlyPro	148
Db	544	AAAGAGCGCGGTGTGATGATTGGCTGTGGCTTGGGTGCATCTCTTGTCTGTGGGCTCT	603
QY	149	MetIleLeuIleSerAspSerTrpGlnAsnSerThrTrp-----GluCyGlu	164
Db	604	GCCATCTTTGTTCTGGCAATACTTTGTAGGAGAAAGAACTGTGCCCCCGAGAAATGTTTC	663
QY	165	ProGlyPheLeuLysTyrTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeuIle	184
Db	664	ATTCAAGTTTCTAAGTAGGACCACCATCACTCTGGACGGGAGATGGCTGCTTTTACATG	723
QY	185	ProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpPserLeuTrpLysArg---	203
Db	724	CTCTGCACCATCATGACTATT-----TTATACTGAGAAATCTATTAGAGACT	771
QY	204	GluIysLeuSerArgCybLeuSer-----	211
Db	772	GAGAAAGCTACCAAAAGAGCTGGCTGGCTACAGGCTGTGGAGACAAAGCGGAAGACAA	831
QY	212	-----HisProValLeuProSerAspSerSerSerSer-----	222
Db	832	AACTTTGTCCACCCCAAGCAGATTTCTGAAGCTGTAGACACTATGAGCTTCAACAGCAA	891
QY	222	-----	222
Db	892	GGCACGAAACGCTATCTAGAGAGAAGTATGTGCTGTCACTTGTGTTCAACACTAAG	951
QY	223	-----AaphIsglyHisSerCybArg-----Gln	230
Db	952	AGCTGGAAGCCAGCTGAGCAGATGAGACCAAGCACACAGTACAGAGACAGTTGCAT	1011
QY	231	AspProAspSerArgAlaThrLeuProAlaArgLysGluThrThrAlaSer-----	247
Db	1012	AACAACAGTGTGCTGCTCTCCCTG-----GAAACTGTGCTTCTTGATGAA	1059
QY	248	-----LeuGlySerAsp-----	251
Db	1060	GAGGATATTGGCTACGAGAACCAAGCCATTTATTCATTGATCACTCAAGCTCCGGGTAT	1119
QY	252	LysSerArgArgLysSerSerLeuLeuProSer-----	262
Db	1120	AGCACCATCTCAACTTACCAAGCTACCTCTCAGATAACTCTGACAGTCCAGACAAAG	1179
QY	263	-----IleArgAlaTyrLys-----	267
Db	1180	GACCTGGGGACTATGATGTAGAGAGAAATGCCATTAAAGCTTCAGGCCCAAGAGATATG	1239
QY	267	-----	267
Db	1240	GATGACCGTGACAACCTGTCAAGAGGACTTCTCCAAAGCTCCCATCAGTTAGAGTCTCC	1299
QY	268	-----AsnSerAsnVal-----	271
Db	1300	GTGACACACAGCCAAAGACTCTTGACACCAACTCTCTGGGTGACAAAGACCAAGCGCGCTTA	1359
QY	272	-----IleAserLysMetGlyPheLeuSerHisSerAsp	283
Db	1360	CCTGTGCTTCAAAAGAAAGCAAGCTGGCTTAAGAGTTTGTGCTCAAGACCAAGAAAGTCA	1419
QY	284	SerLeuAlaLeuGlnArgGlnHisIleGluLeuPheArgAlaArgLysLeuAlaLys	303
Db	1420	-----ATCAACCAAGCGGAAAAAGATGTGCTCATCAAGAGAAAGAGCGCGCCAG	1470

Oy		304	Ser1enulal1euleuLeulAal1aaphal1ileCyser1rhaplabrotyrSerleutThr	323
Db		1471	ACACTGAGTGCACCTTGCTGGCTTCATCATCAAGCGACCCCTTAACAATCAGGTGTC	1530
Oy		324	Vall1eyrSeephePheProgluaYgsmleuthryseThryrh1sthrAla	343
Db		1531	CTGTGTAAACACCTTCTGTGAC-----AGCTGCATTACCACAAACCTATTGGATCTGGGC	1584
Oy		344	PheTrpleuglntprPheanSerPheValAsnProPheleutyPrProleuCysWh1sllys	363
Db		1585	TACTGGCTGTGCTATTATCAACAGCACGCGTAACCCCGTGTATGCCCTGTGCACAAAG	1644
Oy		364	ArgPheglInlysaIaPheleUyls1leleupProval-----	375
Db		1645	ACATTTCGAACACACCTTTCAAGATGCTCTTATGCCAGTGTGACAGAAGAACGGCGGC	1704
Oy		376	-----ArgArgInsSerThrProPheHisAnArg	385
Db		1705	AAACACAGCATTCACGACGACGACGTCCGTCATTTTTTCACAAAGCA	1749
RESULT 6				
AKO80950		3171 bp	mRNA	linear HTC 03-APR-2004
LOCUS				
DEFINITION			Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length	
			emulated library, clone:B430217G05 product:MOSCARINIC ACETYLCHOLINE	
			RECEPTOR M3 (MM3 MACHR), full insert sequence.	
ACCESSION		AKO80950		
VERSION		AKO80950.1	GI:26348896	
KEYWORDS		HTC, CAP trapper.		
SOURCE		Mus musculus (house mouse)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE				
AUTHORS		1	Carninci P. and Hayashizaki Y.	
TITLE			High-efficiency full-length cDNA cloning	
JOURNAL			Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE			99279253	
PUBMED			10349636	
REFERENCE		2	Cerninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,	
AUTHORS			Itoh M., Komoto H., Okazaki Y., Muramatsu M. and Hayashizaki Y.	
TITLE			Normalization and subtraction of cap-trapper-selected cDNAs to	
JOURNAL			prepare full-length cDNA libraries for rapid discovery of new genes	
MEDLINE			Genome Res. 10 (10), 1617-1630 (2000)	
PUBMED			20499374	
REFERENCE			3	
AUTHORS			Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,	
			Komoto H., Akiyama D., Niishi K., Kitamura T., Tashiro H., Itoh M.,	
			Sunji N., Ishii Y., Nakamura S., Hazama M., Nishire T., Harada A.,	
			Yamaneko R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,	
			Fujimake S., Inoue K., Togawa K., Izawa M., Onozaki E., Watanabe M.,	
			Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuyama S., Kawat J.,	
			Okazaki Y., Muramatsu M., Inoue Y., Kita A. and Hayashizaki Y.	
TITLE			RIKEN integrated sequence analysis (RISA) system--384-format	
JOURNAL			sequencing pipeline with 384 multicapillary sequencer	
MEDLINE			Genome Res. 10 (11), 1757-1771 (2000)	
PUBMED			20530913	
REFERENCE			4	
AUTHORS			The RIKEN Genome Exploration Research Group Phase II Team and the	
			FANTOM Consortium.	
TITLE			Functional annotation of a full-length mouse cDNA collection	
JOURNAL			Nature 409, 685-690 (2001)	
AUTHORS			5	
TITLE			The FANTOM Consortium and the RIKEN Genome Exploration Research	
JOURNAL			Group Phase I & II Team.	
AUTHORS			Analysis of the mouse transcriptome based on functional annotation	
			of 60,770 full-length transcripts	
JOURNAL			Nature 420, 563-573 (2002)	
REFERENCE			6	
AUTHORS			(bases 1 to 3171)	
			Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,	

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, D., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohtsuo, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

**TITLE**  
Direct Submission  
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

**COMMENT**  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/.  
Location/Qualifiers

**FEATURES**

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US-10-626-398-10 (1-389) x AK080950 (1-3171)

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1773)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,  
Fertier,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submision  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
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AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Mech. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
TITLE	Itch, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to		
MEDLINE	prepare full-length cDNA libraries for rapid discovery of new genes		
PUBMED			
REFERENCE			
AUTHORS			
TITLE			

JOURNAL MEDLINE PUBMED	Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE	20499374
AUTHORS	11042159
TITLE	3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komoto,H., Akiyama,J., Nishi,K., Kiteunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Mitsuue,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiyagi,K., Fujikake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuda,S., Kawai,D., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
JOURNAL MEDLINE PUBMED	Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
REFERENCE	Genome Res. 10 (11), 1757-1771 (2000)
AUTHORS	20530913
TITLE	11076861
JOURNAL MEDLINE PUBMED	4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium
REFERENCE	Functional annotation of a full-length mouse cDNA collection
AUTHORS	Nature 409, 685-690 (2001)
TITLE	5
JOURNAL MEDLINE PUBMED	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
REFERENCE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
AUTHORS	Nature 420, 563-573 (2002)
TITLE	6 (Bases 1 to 2780)
JOURNAL MEDLINE PUBMED	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanaigaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hitamoto,K., Hirooka,T., Hirose,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kohma,Y., Kondo,S., Konno,H., Koude,M., Koya,S., Kuhiwa,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ono,M., Oshato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Seno,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takebe,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
JOURNAL MEDLINE PUBMED	Muramatsu,M. and Hayashizaki,Y.
REFERENCE	Submitted (16-JULY-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
AUTHORS	Direct Submission
TITLE	CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
JOURNAL MEDLINE PUBMED	Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
REFERENCE	Please visit our web site for further details.
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AUTHORS	70. .1536
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## ORIGIN

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US-10-626-398-10 (1-389) x AK032763 (1-2780)

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Db 1165 ACCAGCATAGAGCCAGGGCTGGGCAAGTCAAGCGAAGCAGAGTCAAGTGGCTG 1224
Qy 285 -----LeuAlaLeuGlnGlnArgGluHisIle----- 293
Db 1225 GACTACATCAAGATCACTGGAAGAGGCTCCGCTCAATTCAGACAGATGTGTCGGG 1284
Qy 294 ---GluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuAlaIleAlaPhe 312
Db 1285 TTGCACCTTGAAACGAGAGCGAAGGCAAGCCAGCAAGATGGAGTTGATCAGGACATTC 1344
Qy 313 AlaIleCysTrpAlaProTyrSerLeuThrValIleTyrSerPhePheProGluArg 332
Db 1345 ATTCTGCTGCGATTCCTCTTATTCATCTTCTCATGTGATGATGATGATGATGATGATGAT 1395
Qy 333 AsnLeuThrLysSerThrTrpTyrHisIleThr--AlaPheTrpLeuGlnIntPheAsnSer 351
Db 1396 AACAGCTGTGCGAGCGAAGCTGTGCAATGTGCAATTTGGTGGCTGCATCACTGCC 1455
Qy 352 PheValAspProPheLeuTyrProLeuCysHisLysAlaArgPheGlnLysAlaPheLeuLys 371
Db 1456 ACCGTGAACCCCTCATCTACCCGCTGTGCAAGAACTTCAAGAAACATTCAAADAA 1515
Qy 372 IleLeuProValArg 376
Db 1516 ATTCTGACATTCGT 1530

```

## RESULT 9

AK047070

LOCUS

DEFINITION

MUS MUSCULUS 10 DAYS NEONATE CEREBELLUM cDNA, RIKEN full-length

enriched library, clone:B930016C09 product: HISTAMINE RECEPTOR H1,

full insert sequence.

ACCESSION

AK047070

VERSION

AK047070.1 GI:26338557

KEYWORDS

MUS MUSCULUS (house mouse)

ORGANISM

MUS MUSCULUS

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Carinci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636  
2  
Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20493574
PMID	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Qy	218	-----	AspSerSerSerSerAspHisGlyHisSerCysArg	-----	Gln	230
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Qy	231	AspPro-----	AspSerArg1aThrLeuProAlaArgGlyGluThrThra1a	246		
Db	968	GACCTTACTGGAGGCTGGATTCAGAAAGTCACACATCTGAAAGACCCCAAGTACCTCTCG	1027			
Qy	247	SerLeuGlySerAspPlySerArgArgLysSerSerLeuLeuProSer11aArg	-----	264		
Db	1028	ACTGCTTTCACCCCAAGAGGGGAAAGGAAACAGTCAACAGCACCCTCTTCCTCGTTGAC	1087			
Qy	264	-----	-----	264		
Db	1088	GTCAATGCACACAGCCTGTGCTGAGGAGATGCCAGGGGCTCAAGGCCAATGACAG	1147			
Qy	265	-----	-----	Ala	265	
Db	1148	ACCTTGAAGCCAGCCCAAAATGGATGAGCAGACCTCGATCTTGTCCGGCGGATCAGTAC	1207			
Qy	266	TyrLysAsnSerAsnVal11a1aSerLysMetGlyPheLeuSerHisSerAspSer	-----	284		
Db	1208	ACATCAGAGACAGACAGCCTGTGGATGCAGCAGTCTTCTCCGGACACAGACTCAGAC	1267			
Qy	284	-----	-----	284		
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Qy	313	Ala1leCysThrP1a1aProTyrSerLeuThrThrVal1leTyrSerPhePheProGluArg	332			
Db	1448	ATTCTGCTGCTGATTCCTCATTTTCACTCTTCAATGAGTCATTTGCTCTGTC	-----	1498		
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Db	1499	AACAGCTCTGCAGGAACTGTGCACATGTTCCACCATTTGGCTGGCTACATCACTCC	1558			
Qy	352	PheValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLys	371			
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RESULT 10						
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LOCUS						
DEFINITION		Mus musculus adult male hypothalamus cDNA, RIKEN full-length				
		enriched library, clone:A230019E03 product:HISTAMINE RECEPTOR H1,				
		full insert sequence.				
ACCESSION		AK038480				
KEYWORDS		AK038480.1 GI:26332590				
FEATURES		HTC; CAP trapper.				
SOURCE		Mus musculus (house mouse)				
ORGANISM		Mus musculus				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE		1 Carninci, P. and Hayashizaki, Y.				
AUTHORS		High-efficiency full-length cDNA cloning				
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE		99279253				
PUBMED		10349636				
REFERENCE		2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,				

TITLE	Normalizaton and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	20499374
REFERENCE	11042159
AUTHORS	3 Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,Y., Nishi,K., Kitanai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaiguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Irawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
JOURNAL	RIKEN Integrated sequence analysis (RISA) system--384-format
MEDLINE	sequencing pipeline with 384 multipicillary sequencer
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE	20530913
AUTHORS	11076861
TITLE	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
JOURNAL	Functional annotation of a full-length mouse cDNA collection
REFERENCE	Nature 409, 685-690 (2001)
AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2979)
AUTHORS	Adachi,U., Aizawa,K., Akimura,T., Arikawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiroaka,T., Hirozane,T., Horii,F., Imoto,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akehira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsunumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details.
SOURCE	URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/ Location/Qualifiers 1..2979 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM.DB:A230019B03" /db_xref="taxon:10090" /clone="A230019B03" /sex="male" /tissue_type="hypothalamus" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 269..1735 /note="unlabeled protein product; HISTAMINE RECEPTOR H1

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## ORIGIN

## Alignment Scores:

Pred. No.:	1,13e-29	Length:	2979
Score:	402.00	Matches:	117
Percent Similarity:	41.44%	Conservative:	84
Best Local Similarity:	24.12%	Mismatches:	164
Query Match:	19.74%	Indels:	120
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US-10-626-398-10 (1-389) x AK038480 (1-2979)

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QY 221 AspPro-----AspSerArgAlaThrLeuProValArgLysGluThrAla 246
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QY 372 IleLeuProValArg 376
DB 1715 ATTCTGCACATTCTGT 1729
RESULT 11
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AK046607 LOCUS Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length
AK046607 DEFINITION enriched library, clone:B430204G09 product: HISTAMINE RECEPTOR H1,
AK046607 full insert sequence.
AK046607 ACCESSION
AK046607.1 GI:26338238
AK046607 VERSION
HTC; CAP trapper.
HTC; CAP trapper. KEYWORDS
Mus musculus (house mouse)
Mus musculus SOURCE
Mus musculus ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning
AUTHORS Meth. Enzymol. 303, 19-44 (1999)
JOURNAL
99279253
MEDLINE
10349636
PUBMED
```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
AUTHORS  
3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishii, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishida, K., Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, T., Okazaki, Y., Murakatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed capillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
AUTHORS  
4  
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
AUTHORS  
5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

TITLE  
JOURNAL  
AUTHORS  
6 (bases 1 to 3783)  
Aachi, U., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Ohata, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Murakatsu, M., and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
Location/Qualifiers

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ORIGIN  
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US-10-626-398-10 (1-389) x AK046607 (1-3783)  
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QY 218 -----AspSerSerSerAspHisGlyHisSerCysArg-----Gln 230
DB 982 GAGGGTCCCAAGAAACCTGGGAAAGATCTCCCTGGGGGGTCCAGAAAGGGCGCTCAAA 1041
QY 231 AspPro-----AspSerArgAlaThrLeuProAlaArgIleGlnThrAla 246
DB 1042 GACCCCTACGAGAGTGTGATCGAAGTCAACATCGAAGACCCCAAGCTGACTCTCG 1101
QY 247 SerLeuGlySerAspIysSerArgIlySerSerLeuIeuProSerIleArg----- 264
DB 1102 ACTGCTTCAGCCAGAGGGGAAAGGAAAGACATCACAGCCCTGTTCCGTCCTTGAC 1161
QY 264 ----- 264
DB 1162 GTCATGACAGACACAGCCTGTGCTGAGGAGATGCCAGGGGCTCAAGGCCAATGACAG 1221
QY 265 -----Ala 265
DB 1222 ACCTTGAGCCAGCCCAATGATGACGAGCCTGACTTCCGGGGGATCAGTGCAG 1281
QY 266 TyrIysAsnSerAsnValIleAlaSerIysMetGlyPheLeuSerHisSerAspSer--- 284
DB 1282 ACATCAGAGACACAGACCTTGCTGATCGACAGTCTCTCCCGGACACAGACTCAGAC 1341
QY 284 ----- 284
DB 1342 ACCAGCATGAGCCAGCGGCTGGGCAAAATGCAAGCAGACAGCTTACAGTGGCCTG 1401
QY 285 -----LeuAlaLeuGlnIleArgGlnHisIle----- 293
DB 1402 GACTACATCAAAATGACCTGGAAGAGGCTTCGCTGCATTCACAGACAGATGATGTCGGG 1461
QY 294 ---GluLeuPheArgAlaArgIlyLeuAlaIlySerLeuAlaIleLeuLeuAlaIle 312
DB 1462 TTGCACTTGAACCGAGAGCGGAAAGGACGACAGACTTGGTGTATCATGTCAGACTTC 1521
QY 313 AlaIleCysThrAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
DB 1522 ATTCCTGCTGGATTCCTCATTTTCATCTTCTTCATGTCATGCTCTTCGC----- 1572
QY 333 AsnLeuThrIlySerThrTyrTyrHisThr---AlaPheTrpLeuGlnIlePheAsnSer 351
DB 1573 AACAGCTGTCGACGGAACCTGTGCACATGTCACCATTTGGCTGGGCTACATCACTTC 1632
QY 352 PheValAsnProPheLeuTyrProLeuCysHisIlyAsnArgPheGlnIlyAlaPheLeuIys 371
DB 1633 ACGCTGAACCCCTCATCTTACCCGCTGTGCACAGAACCTTCAAGAAAGACATTCAAAA 1692
QY 372 IleLeuProValArg 376
DB 1693 ATTCTGCACATTCGT 1707

RESULT 12
LOCUS CD326085 853 bp mRNA linear EST 28-MAY-2003
DEFINITION AGENCOURT_14163426 NICHDP_XGC_Bye1 Xenopus laevis cDNA clone
IMAGE:6949081 5', mRNA sequence.
ACCESSION CD326085
VERSION CD326085.1 GI:31090416
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 853)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
```

```
COMMENT
Contact: Daniela S. Gerthard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgsapb-remail.nih.gov
Tissue Procurement:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM14564 row: F column: 24
High quality sequence stop: 707.
Location/Qualifiers
1..853
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
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/clone_lib="NICHDP_XGC_Bye1"
/note="Organ: eye; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ALIGNMENT
Alignment Scores:
Pred. No.: 9,096-30 Length: 853
Score: 394.50 Matches: 75
Percent Similarity: 73.38% Conservative: 27
Best Local Similarity: 53.96% Mismatches: 36
Query Match: 19.38% Indels: 1
DB: 6 Gaps: 1

US-10-626-398-10 (1-389) x CD326085 (1-853)
QY 15 IleserLeuThrPheLeuMetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValVal 34
DB 382 GTCTTCCTGGCTGCTCTGATGGGGGTCTCATATGACACCGCTGGGGAATGCCCTG 441
QY 35 ValIleLeuAlaPheIleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu 54
DB 442 GTCATGCTGGCTTTGTTGTGTGACATCCAGCCCTCCGACACCAAGAAATATTTCTTCTTC 501
QY 55 AsnLeuAlaIleAlaAspPhePheValGlyAlaIleAlaIleProLeuTyrIleProSer 74
DB 502 AACCTGGCTATCTCAGATTTCTTTAGTGTGCCCTGTGCATCCCTGTATGTGCATPAC 561
QY 75 SerLeuThr---TyrTrpThrSerGlyIysGlnAlaCysValPheTrpLeuIleThrAsp 93
DB 562 GTACTGACTGCGAGATGAGCTTTGGCAGAGCGTTTCCAAACTGTGCTGGCTTGTGAT 621
QY 94 TyrLeuLeuCysThrAlaSerValTyrAsnIleValIleLeuIleSerTyrAspArgTyrGln 113
DB 622 TATCGCTCTGCACTCGCTCCGTGTTCAACATCGTGCATCAGCTACGACAGCTTCAAC 681
QY 114 SerValSerAsnAlaValTyrTyrArgAlaGlnHisSerGlyThrTrpIlyIleAlaThr 133
DB 682 TCTGTGACCCCGGCTGTCAGTTACCGACCTCAGCAGAGTAACACCGCGCATCAGTCTTG 741
QY 134 GlnMetValAlaValTyrIlePheSerPheMetThrAsnGlyProMetIleLeuIle 152
DB 742 AAAATGACCATGCTGTGATCTTGCTTCTCTTATATGACACGACCATTAATATA 798

RESULT 13
LOCUS CB556920 672 bp mRNA linear EST 02-APR-2003
DEFINITION AMGNNUC:UNGPI-00001-D6-A utrgpl (14349) Rattus norvegicus cDNA clone
utrgpl-00001-d6 5', mRNA sequence.
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ACCESSION CB556920  
 VERSION CB556920.1 GI:29496320  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 REFERENCE 1 (bases 1 to 672)  
 AUTHORS Amgen EST Program.  
 TITLE Amgen Rat EST Program  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Dan Fitzpatrick  
 Amgen, Inc  
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Plate: 00001 row: d column: 6.  
 Location/Qualifiers  
 1..672  
 /organism="Rattus norvegicus"  
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## ORIGIN

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 Pred. No.: 1,27e-29 Length: 672  
 Score: 391.50 Matches: 79  
 Percent Similarity: 67.95% Conservative: 27  
 Best Local Similarity: 50.64% Mismatches: 43  
 Query Match: 19.23% Indels: 7  
 DB: 6 Gaps: 3

US-10-626-398-10 (1-389) x CB556920 (1-672)

QY 3 AlAsnAsnSerThrIleAlaLeuThrSerIleYrIleSerLeuThrPheLeuMetSer 22  
 DB 194 GCGCGCGGCTTCGCGCTGCGACCGCTGC-----CTGGCTGCGCTCATGGCG 244  
 QY 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42  
 DB 245 CTGCTCATCTGCGCCACAGACTGGGCAAGCGCGTGTCTATGCTCGCTTCGTGGCGGAT 304  
 QY 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhe 62  
 DB 305 TCGAGCTCCGACCCAGACCACTTCTTCTGCTCAACTCGGCATCTCCGACTTCTC 364  
 QY 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr--TyrTTPThrSer 81  
 DB 365 GTGGGTGCTTCGTCATCTCCATTCGTAACCTATGCTGTGACCGCGCTTGGACCTTC 424  
 QY 82 GlyLeuGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 101  
 DB 425 GGGCGGGGCTTCGCAAGCTGTGCTGTGTAGACTACTGATGCTCTCTCGCTC 484  
 QY 102 TyrAsnIleValIleLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTTPYr 121  
 DB 485 TTCACATCTGACTCATCATGACCTATGACCGATTCCTGTGACGACTGCTCTCTAC 544  
 QY 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTTPIlePhe 141  
 DB 545 AGGGCCCGAGGGGACACAGACGGCGCTTCGAGAGATGACATGCTGTGGTGTCTG 604  
 QY 142 SerPheMetThrAsnGlyPromerIleLeuIleSerAspSerTyrGln 157  
 DB 605 GCCTTCTGCTGATGGGCTGCATCTG-----AGTTGGAG 643  
 RESULT 14  
 AY399428  
 LOCUS AY399428 1401 bp DNA linear GSS 15-DEC-2003

DEFINITION Mus musculus ADRA1A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY399428  
 VERSION AY399428.1 GI:39755417  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1401)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302

REFERENCE 2 (bases 1 to 1401)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

## FEATURES

source  
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## ORIGIN

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 Score: 391.00 Matches: 117  
 Percent Similarity: 44.39% Conservative: 61  
 Best Local Similarity: 29.18% Mismatches: 139  
 Query Match: 19.20% Indels: 84  
 DB: 9 Gaps: 16

US-10-626-398-10 (1-389) x AY399428 (1-1401)

QY 4 AsnAsnSerThrIleAlaLeuThrSerIleYrIleSerLeuThrPheLeuMetSerLeu 23  
 DB 34 TCBACTGCACCCACCGCCAGACAGTGAACATTTCTAAGCCATTTCTATGGGGTG 93  
 QY 24 -----LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPhe 39  
 DB 94 ATCTGGGGGCTTCATCATTTTCGGGTCCTTGGGAATTTAAGATCACTCGGTG 153  
 QY 40 IleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAla 59  
 DB 154 GCCTGTCACTGGCATTTGCACTGTGATCACTACTACTTGTCAACCTGCGTGTGCA 213  
 QY 60 AspPhePheValGlyAlaIleAlaIleProLeu--TyrIleProSerSerLeuThrTyr 78  
 DB 214 GACTCTCTCTCACTCCACCGCTGCTCTCTCTGCACTTTTGAATCCCTGGGTAC 273  
 QY 79 TrpThrSerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThr 98  
 DB 274 TGGGCTTTGGCAGGGTGTCTGCAACATCTGGCGCGGTGACGCTTATCTGCACA 333  
 QY 99 AlSerValTyrAsnIleValIleLeuIleSerTyrAspArgTyrGlnSerValSerAsnAla 118  
 DB 334 GCGTCATCATGGGCTTCGTCATCTCCATGACCGATCACTTGTGTGACTACCCG 353  
 QY 119 ValTrpTyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGln----- 134

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Db      394 CTGCGCTACCCACC-----ATGTGACCCAGAGGAGGCGCGTC 432
Qy      135 -----MetValAlaValTrpIlePheSerPheMetThrAsn---GlyProMetIleLeu 151
Db      433 AGGGCTCTGCTCTGCGCTGGCGGCTTTCTTGGTCATCTCCATCGAGACCCCTGTC--- 489
Qy      152 IleserAspSerTrpGlnAsnSerThrTrgIu-----Cys----- 163
Db      490 -----GGCTGGAGGAGCAGAGGCTCCGAGGATGACCATCGCAATTCATGATGAG 540
Qy      164 GIuProGlyPheLeuYelYelTrpTrpPheAlaLeuProThSerLeuLeuGluPheLeu 183
Db      541 GAGCCAGGATACGTCG-----CTGTTCTCAGCGCTGGCGCTTTCTTCAC 582
Qy      184 ILeProIleLeuLeuValAlaTrpPheSerAlaHisIleTrpSerLeuTrpIlyAsp 203
Db      583 GTGCCACTGACCATCATCTCTGTTATGTACTGTCCAGTCTAC---GTGCTACCCAGAGA 639
Qy      204 GIuYsLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223
Db      640 GAA-----AGCCGAGGCTCAAGTCGGC---CTCAAGACCCGACAGTCAAGTCAAGAG 690
Qy      224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgYsGlu 243
Db      691 -----CAAGTGACGCTCCGTATCCACCGCTAAA 717
Qy      244 ThrThrAlaSerLeuGlySerAspIlySerAspIlySerArgYsSerSerLeuLeuProSerIle 263
Db      718 AATGTCCTCCGCAAGAGCGGAGGAGTACAGTACCCAGAAATTAAGTCACTCTTCCTCG 777
Qy      264 ArgAlaTrpYsAsnSerAsnValIleAlaSerIlyMetGlyPheLeuSerHisSerAsp 283
Db      778 AGCGTGTCTCAAGTTTCC----- 795
Qy      284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgYsLeuAlaYs 303
Db      796 -----CGAGAGAAAGAAACCCGCAAG 816
Qy      304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTrpSerLeuThrTr 323
Db      817 AGCGTGGGATTTGGTGGAGATGCTTCCTGCTGCTGCTGCTGCTGCTTCTTCTTCCTCG 876
Qy      324 ValIleTrpSerPhePheProGluArgAsnLeuThrIlySerThrTrpTrpHisThrAla 343
Db      877 CCCATTGGGATCTTCTTCCGGAATTTCAAG---CCACCGGAAACAGTTTCAAAATAGTA 933
Qy      344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTrpProLeuYsHisIly 363
Db      934 TTTTGCTTGGGTACTAATATAGTTGCATCAACCCCTATCATATACCATCCAGTCCAGCC 993
Qy      364 ArgPheGlnIlyAlaPheLeuYsIleLeuProVal-----ArgArgGlnSer 379
Db      994 GAGTTTCAAGAAAGCTTTTCAGAATGTGCTGCCAATTCATGCTTCTTCGAGAGGAGCT 1053
Qy      380 Thr 380
Db      1054 TCC 1056

```

```

RESULT 15
AK085653 4124 bp mRNA linear HTC 03-APR-2004
LOCUS AK085653 Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
DEFINITION library, clone:ID630050N06 product:adrenorenergic receptor, alpha 1a,
ALPHA 1A-ADRENORECEPTOR, full insert sequence.
ACCESSION AK085653
VERSION AK085653.1 GI:26351716
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1

```

```

AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multiplexed sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
MEDLINE 11076861
PUBMED 11076861
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 11076861
PUBMED 11076861
REFERENCE 6
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, P., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail: genome-research@riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
FEATURES
source location/Qualifiers
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CDs

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Score: 391.00 Matches: 117  
Percent Similarity: 44.39% Conservative: 61  
Best Local Similarity: 29.18% Mismatches: 139  
Query Match: 19.20% Indels: 84  
DB: 3 Gaps: 16

US-10-626-398-10 (1-389) x AK085653 (1-4124)

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DB 986 TCCAACTGCACCCGACCCGACGACAGTGAACATTTCTTAAGCCATTCCTGGGCTG 1045
QY 24 -----LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPhe 39
DB 1046 ATCTGGGGGGCTCATATTTTCGGGGTCTGGGGAATATTAGATCTCTCGGTG 1105
QY 40 IleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAlaIleAla 59
DB 1106 GCCTGCATGCGATCGACCTCGTGACTCACAACATTCGCACTGGCTGGTGGCA 1165
QY 60 AspPhePheValGlyAlaIleAlaIleProLeu---TyrIleProSerSerLeuThrTyr 78
DB 1166 GACCTCTCTCACTCACTCACTGCTGCTCTCTCTGCAATCTTTGAGATCTGGGCTAC 1225
QY 79 TrpThrSerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrIleLeuCysThr 98
DB 1226 TGGGCTTGGGAGGGTCTTGCAACATCGGGCGGGGAGCGCTTATGCTGCACA 1285
QY 99 AlSerValTyrAsnIleValIleSerTyrAspArgTyrGlnSerValSerAsnAla 118
DB 1286 GCGTCCATCGAGGCTCTCATCATCTCATCGACCGATACATGGTGTGAGCTACCCG 1345
QY 119 ValTrpTyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGln----- 134
DB 1346 CTGGCGTACCCACAC-----ATTGTCACCCACAGAGAGGGGGGCTC 1384
QY 135 -----MetValAlaValTrpIlePheSerPheMetThrAsn---GlyProMetIleLeu 151
DB 1385 AGGGCTCTGCTGCTGCTGGGCGCTTCTGTCATCTCCATCGAGACCCCTGTTC--- 1441
QY 152 IleSerAspSerTyrGlnAsnSerThrThrGlu-----Cys----- 163
DB 1442 -----GCTGGAGGACAGGAGCTCCGAGGATGAGACCATCTGCCAAATCAATGAG 1492
QY 164 GluProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 163

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DB 1493 GAGCCAGGATACGTG-----CTGTCTCAAGCGCTGGGCTCTTCTAC 1534
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuThrLysArg 203
DB 1535 GTGCCACTGACCACTCATCTGTTATGATCTGTGAGATCTAC---GTGGTAAGCCAAAGGA 1591
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 1592 GAA-----AGCCGAGGCTCAAGTCCGGC---CTCAAGACCAAGTACACTCAGAG 1642
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
DB 1643 -----CAAGTACGCTCCGTATCAACCGTAA 1669
QY 244 ThrThrAlaSerLeuGlnTyrSerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
DB 1670 AATGTCCTGCAGAAAGCAGCGAGTGAAGCAGTGCAGAAATGAAGTCACTTCTCCGTG 1729
QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 1730 AGGCTGCTCAAGTTTTC----- 1747
QY 284 SerLeuAlaLeuGlnGlnArgGlnHisIleGlyLeuPheArgAlaArgLysLeuAlaLys 303
DB 1748 -----CGAGAGAAAGAAAGCCGCAAG 1768
QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerSerLeuThr 323
DB 1769 ACCCTGGGCATTGTGGTGGGATGCTTCCTGCTGGCTGGCTGCATTCTTCCTCGATG 1828
QY 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrGlnHisThrAla 343
DB 1829 CCAATGGGCTCTCTTCCGAAATTCAAG---CAACGGAAACAGTTTCAAAATAGTA 1885
QY 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
DB 1886 TTTTGGCTTGGTACCTAAATAGTTGCATCAACCATCATATACCATGCTCCAGGCAG 1945
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProVal-----ArgArgGlnSer 379
DB 1946 GAGTTCAAGAAACCTTTTCAGAAATGCTGCGAATCCAGTGTCTTGCAGAAAGCAGTCT 2005
QY 380 Thr 380
DB 2006 TCC 2008

```

Search completed: August 5, 2005, 22:50:04  
Job time : 3191 sec

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 01:44:58 / Search time 172 Seconds  
(without alignments)  
1158.133 Million cell updates/sec

Title: US-10-626-398-10

Sequence: 1 MLANNSTIALTSIKISLTF.....LKILPVROSTPPHNRISST 389

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2025	99.5	389	2	Q91ZY3 cavia porce
2	1310.5	64.4	390	2	Q96LD9 096149 homo sapien
3	1308.5	64.3	390	1	HH4R_HUMAN 09h38 homo sapien
4	1244	61.1	391	2	Q91ZY2 mus musculu
5	1235.5	60.7	391	2	Q91ZY1 ratu
6	1221.5	60.0	390	2	Q8WNV9 08wnv9 sus scrofa
7	693	34.0	445	1	HH3R_CAVPO 09j135 cavia porce
8	689.5	33.9	445	1	HH3R_HUMAN 09y5n1 homo sapien
9	688.5	33.8	445	2	Q86SE1 0865e1 macaca mula
10	681.5	33.5	445	1	HH3R_RAT 09qy8 ratu
11	679.5	33.4	445	1	HH3R_MOUSE 09h38 mus musculu
12	666	32.7	473	2	Q6ZM33 06zm33 brachydantio
13	655.5	32.2	365	2	Q8WY01 08wy01 homo sapien
14	655.5	32.2	373	2	Q8WY02 08wy02 homo sapien
15	534.5	26.3	174	2	Q6J9J4 06j9j4 gorilla gor
16	528.5	26.0	175	2	Q6J9J5 06j9j5 pan troglod
17	472	23.2	301	2	Q8WY00 08wy00 homo sapien
18	472	23.2	309	2	Q8N149 08n149 homo sapien
19	414	20.3	639	1	ACM3_CHICK 09578 gallus gall
20	413.5	20.3	590	1	ACM3_BOVIN 09194 caenothabdi
21	413	20.3	585	1	ACM3_CAREL 09u745 caenothabdi
22	410	20.1	486	1	HH1R_RAT 09i30 ratu
23	408.5	20.1	589	1	ACM3_RAT 09i30 ratu
24	407.5	20.0	528	2	Q9PT66 09pt66 gallus gall
25	406	19.9	488	1	HH1R_CAVPO 09i38 gallu
26	405.5	19.9	590	1	ACM3_PONPY 09n232 pong
27	404.5	19.9	589	1	ACM3_MOUSE 09n232 mus musculu
28	404	19.8	488	2	Q91V49 09i49 mus musculu
29	403.5	19.8	590	1	ACM3_GORGO 09n23 gorilla gor
30	403.5	19.8	590	1	ACM3_HUMAN 09n23 gorilla gor
31	403.5	19.8	590	1	ACM3_HUMAN 09n23 gorilla gor

32	403.5	19.8	590	1	ACM3_PANTR	Q9n244 pan troglod
33	402.5	19.8	531	1	ACM5_RAT	P08911 ratu
34	402	19.7	488	1	HH1R_MOUSE	P70174 mus musculu
35	402	19.7	488	2	Q91V66	Q91v66 ratu
36	402	19.7	564	2	Q96RG9	Q96rg9 homo sapien
37	400	19.6	611	2	Q7JKV1	Q7jkv1 caenothabdi
38	399	19.6	587	2	Q8VH26	Q8vh26 cavia porce
39	395.5	19.4	487	2	Q9N2B1	Q9n2b1 gorilla gor
40	395.5	19.4	532	1	ACM5_HUMAN	P08912 homo sapien
41	395	19.4	480	2	Q7T286	Q7t286 brachydantio
42	394.5	19.4	530	2	Q8VH24	Q8vh24 cavia porce
43	393.5	19.3	532	2	Q81VW0	Q81vw0 homo sapien
44	392	19.3	466	1	A1AA_RAT	P43140 ratu
45	391.5	19.2	425	2	Q9WZU2	Q9wzu2 oryctolagus

ALIGNMENTS

RESULT 1

Q91ZY3 PRELIMINARY; PRT; 389 AA.

AC Q91ZY3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histamine H4 receptor.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AF358858; AAK97379.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHOPOPSN.  
DR PRINTS; PR01726; HISTAMINEH4R.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 389 AA; 44511 MW; 51AR32FD6FIC3E4F CRC64;

Query Match 99.5%; Score 2025; DB 2; Length 389;  
Best Local Similarity 99.7%; Pred. No. 1.2e-128;  
Matches 388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MLANNSTIALTSIKISLTFMSLALAIMGNVVIILAFVDRNLHRNSYFFLNLAIAD	60
DB	1	MLANNSTIALTSIKISLTFMSLALAIMGNVVIILAFVDRNLHRNSYFFLNLAIAD	60
QY	61	FFVGAIAPIPIYSSITVWTSGKACVFWLITDYLLCTASVNIIVLISYDRYOSVSNVW	120
DB	61	FFVGAIAPIPIYSSITVWTSGKACVFWLITDYLLCTASVNIIVLISYDRYOSVSNVW	120
QY	121	YRQSHGWTWIAIQAQVAWVLFSPFTMGPMILISDSWQNSTTECPGLKMYFALPSSL	180
DB	121	YRQSHGWTWIAIQAQVAWVLFSPFTMGPMILISDSWQNSTTECPGLKMYFALPSSL	180
QY	181	EFILIPILVAVFSAHIYWSLMKREKLSRCLSHFVLPSDSSSDHGHSCRODPSPRATLPA	240
DB	181	EFILIPILVAVFSAHIYWSLMKREKLSRCLSHFVLPSDSSSDHGHSCRODPSPRATLPA	240
QY	241	RKETTASLGSDDRKRKSLPSIRAYKNSNVIAKMGFLSHSOSLALQOREHIELPRARK	300
DB	241	RKETTASLGSDDRKRKSLPSIRAYKNSNVIAKMGFLSHSOSLALQOREHIELPRARK	300

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QY 301 LAKSLAIIILAAFAICWAPSLTTVIYSPFPERNLTKSTWYHTAFMLQWNSFVNPLYL 360
DB 301 LAKSLAIIILAAFAICWAPSLTTVIYSPFPERNLTKSTWYHTAFMLQWNSFVNPLYL 360
QY 361 CHKRFOKAFKILPVRROSTPPHNRISIT 389
DB 361 CHKRFOKAFKILPVRROSTPPHNRISIT 389

RESULT 2
ID 096ID9 PRELIMINARY; PRT; 390 AA.
AC 096ID9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Histamine receptor H4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21106319; PubMed=11179435;
RA Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R.,
RA Rauber L., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RT "Discovery of a novel member of the histamine receptor family.";
RL Mol. Pharmacol. 59:427-433(2001).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR InterPro; IPR008102; Histamine_recept_H4.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopn.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0282; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 390 AA; 44469 MW; CC82B5D30D216C66 CRC64;
SQ

Query Match 64.4%; Score 1310.5; DB 2; Length 390;
Beet Local Similarity 64.7%; Pred. No. 1.7e-80;
Matches 253; Conservative 48; Mismatches 87; Indels 3; Gaps 3;
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QY 360 LCHKRFOKAFKILPVRROSTP-PHNRISIT 389
DB 360 LCHKRFOKAFKILPVRROSTP-PHNRISIT 389
DB 360 LCHKRFOKAFKILPVRROSTP-PHNRISIT 389

RESULT 3
ID HH4R HUMAN STANDARD; PRT; 390 AA.
AC 09H3N8; 09GZ00;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)
DE (GPCR105) (SP9144) (AXOR35).
GN Name=HH4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20538417; PubMed=10973974; DOI=10.1074/jbc.M006480200;
RA Oda T., Morikawa N., Saito Y., Masuno Y., Matsumoto S.-I.;
RT "Molecular cloning and characterization of a novel type of histamine
RT receptor preferentially expressed in leukocytes.";
RL J. Biol. Chem. 275:36781-36786(2000).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=leukocyte;
RX MEDLINE=20568725; PubMed=1118334; DOI=10.1006/birc.2000.4008;
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
RT "Molecular cloning and characterization of a new human histamine
RT receptor, HH4R.";
RL Biochem. Biophys. Res. Commun. 279:615-620(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Jones P.G., Wu S., Betty M.;
RT "Cloning of a novel histamine receptor.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=bone marrow;
RX PubMed=11179434;
RA Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J.,
RA Pyati J., Li X., Chai W., Caruthers N., Lovenberg T.W.;
RT "Cloning and pharmacological characterization of a fourth histamine
RT receptor (H4) expressed in bone marrow.";
RL Mol. Pharmacol. 59:420-426(2001).
RN [5]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=eosinophil;
RX MEDLINE=2110636; PubMed=11181941;
RA More K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,
RA Antles J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,
RA Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,
RA Monma F.J. Jr.;
RT "Cloning and characterization of a novel human histamine receptor.";
RL J. Pharmacol. Exp. Ther. 296:1058-1066(2001).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21106320; PubMed=11179436;
RA Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dycko G.M., Mannan I.J.,
RA Boyer R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,
RA Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,
RA Bergsma D.J., Fitzgerald L.R.;
RT "Cloning, expression, and pharmacological characterization of a novel
RT human histamine receptor.";
RL Mol. Pharmacol. 59:434-441(2001).
RN [7]
RP SEQUENCE FROM N.A.
RA O'Reilly M.A.;
RT "Identification of a histamine H4 receptor on human eosinophils - Role
```

RT in eosinophil chemotaxis." ;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Puhl H.L., Iikeda S.R., Aronstam R.S.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: The H4 subclase of histamine receptors could mediate the  
 CC histamine signals in peripheral tissues. Displays a significant  
 CC level of constitutive activity (spontaneous activity in the  
 CC absence of agonist).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and  
 CC eosinophils. Shows preferential distribution in cells of  
 CC immunological relevance such as T-cells, dendritic cells,  
 CC monocytes, mast cells, neutrophils. Also expressed in a wide  
 CC variety of peripheral tissues, including the heart, kidney, liver,  
 CC lung, pancreas, skeletal muscle, prostate, small intestine,  
 CC spleen, fetal liver and lymph node.  
 CC -1- INDUCTION: Expression is either up-regulated or down-regulated  
 CC upon activation of the lymphoid tissues and this regulation may  
 CC depend on the presence of IL-10 or IL-13.  
 CC -1- MISCELLANEOUS: Does not bind diphenhydramine, loratadine,  
 CC ranitidine, cimetidine and chlorpheniramine. Shows modest affinity  
 CC for dimaprit, imipromidine, clobenpropit, thioferamide, burimamide  
 CC clobazepam, imipipit and imetit. The order of inhibitory activity  
 CC was imetit > clobenpropit > burimamide > thioferamide.  
 CC Clobenpropit behaves as a partial agonist, dimaprit and  
 CC imipromidine show some agonist activity while clobazepam behaves as  
 CC a full agonist. Thioferamide shows inverse agonism (enhances CAMP  
 CC activity). The order of inhibitory activity of histamine  
 CC derivatives was histamine > N-alpha-methylhistamine > R(-)-alpha-  
 CC methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-  
 CC methylhistamine > R(-)-alpha-methylhistamine behave as full  
 CC agonists.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation-  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AB044934; BAB13698.1; -;  
 CC EMBL: AB045370; BAB20091.1; -;  
 CC EMBL: AF307973; AAC32052.1; -;  
 CC EMBL: AF312330; AAK12081.1; -;  
 CC EMBL: AF329449; AAK43542.1; -;  
 CC EMBL: AF329556; AAL01684.1; -;  
 CC EMBL: AJ298292; CAC83493.1; -;  
 CC EMBL: AY136745; AAN01271.1; -;  
 CC PIR: JCT566; JCT566.  
 CC Genew: HGNC:17383; HRH4.  
 CC MIM: 606792; -;  
 CC GO: GO:0016021; C: integral to membrane; NAS.  
 CC GO: GO:0004569; F: histamine receptor activity; NAS.  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC InterPro: IPR008102; Histamrecept\_H4.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS: PRO00237; GPCRHOOPS.  
 CC PRINTS: PRO1726; HISTAMINHR4.  
 CC PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 CC PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 CC DR G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
 CC Transmembrane.  
 CC KM Transmembrane.  
 CC FT DOMAIN 1 19 Extracellular (Potential).  
 CC TRANSMEM 20 40 1 (Potential).  
 CC DOMAIN 41 52 Cytoplasmic (Potential).  
 CC TRANSMEM 53 73 2 (Potential).  
 CC FT 74 87 Extracellular (Potential).  
 CC DOMAIN

FT TRANSMEM 88 108 3 (Potential).  
 FT DOMAIN 109 131 Cytoplasmic (Potential).  
 FT TRANSMEM 132 152 4 (Potential).  
 FT DOMAIN 153 172 Extracellular (Potential).  
 FT TRANSMEM 173 193 5 (Potential).  
 FT DOMAIN 194 304 Cytoplasmic (Potential).  
 FT TRANSMEM 305 325 6 (Potential).  
 FT DOMAIN 326 341 Extracellular (Potential).  
 FT TRANSMEM 342 362 7 (Potential).  
 FT DOMAIN 363 390 Cytoplasmic (Potential).  
 FT DISULFID 87 164 By similarity.  
 FT CARBOHYD 5 9 N-linked (GlcNAc... ) (Potential).  
 FT LIPID 374 374 N-linked (GlcNAc... ) (Potential).  
 FT CONFLICT 138 138 S-palmitoyl cysteine (Potential).  
 FT CONFLICT 206 206 A -> V (in Ref. 1).  
 FT CONFLICT 253 253 H -> R (in Ref. 1).  
 SQ SEQUENCE 390 AA: 44495 MW: C986B8AE7FE912C3 CRC64;  
 Query Match 64.3%; Score 1308.5; DB 1; Length 390;  
 Best Local Similarity 65.1%; Pred. No. 2,3e-80;  
 Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;  
 QY 5 NSTIALT-SIKISLTFELSLAIAIMLGNVVIATFVDRNLRHSNYFFLNLAIADFPV 63  
 DB NSTINLSLSTRTVLAFFMSLVAFALMGNALVILAFVVDKNLRHSYFFLNLAIADFPV 64  
 QY 64 GAIALIPYPSLSITTSYSGKACVFELITDYLLCTSYNNIVULSIDRQSVSNATWYRA 123  
 DB GVSIISIPYIPHLTFENDFKELICVFWLITDYLLCTSYNNIVULSIDRSLVSNAYSRT 124  
 QY 124 QHSCTKIKITOMAVAVIFSPMTNGPMILISDSQNSTCEPGLKMYFALPTSLLEFL 183  
 DB QHTGVAKITLWAVAVLAFVNGPMILVSESKDGSCEPFESEWIIATTSLEEV 184  
 QY 125 QHTGVAKITLWAVAVLAFVNGPMILVSESKDGSCEPFESEWIIATTSLEEV 184  
 QY 184 IPIILVAYFSAHITWYSLMKREKLSRCLSHPVLPSSDSSSDHGHSCRODPSRATLPARKE 243  
 DB IPVILVAYFNMNIYSLMKRDHLRSCSHPLGLA-VSSNICGHSFGRSLSRSLASTE 243  
 QY 244 TTSLSGDSRRKSLSPSTRAYKNVVASKKGFLSHSDSLAOREHELFRAKTLK 303  
 DB VPSFSEQRKSSIMFSSRTKMSNTIASKKGSPSDSVALLHREHVELLRARLAK 303  
 QY 304 SLAIIAARFACAPASLTIVYSPFERNLTKSTYTHAFVWLQWNSFVNPLYPICRK 363  
 DB SLAIIIGVAVCAVAPSLSTIVYSATGPKSVYRIAFWLQWNSFVNPLYPICRK 363  
 QY 364 RFOKAFKLIPVRRQSTP-PHNRSIST 389  
 DB RFOKAFKLIFCIKOPLPQSHRSVSS 390  
 RESULT 4  
 ID Q912Y2 PRELIMINARY; PRT; 391 AA.  
 AC Q912Y2;  
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
 DT 01-DEC-2001 (T-EMBLrel. 19, last sequence update)  
 DE 01-OCT-2003 (T-EMBLrel. 25, last annotation update)  
 GN Histamine H4 receptor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=BALB/C;  
 RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ database.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL: AF358859; AAK97380.1; -;

DR MGD; MGI:2429635; Hrh4.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0005887; C:integral to plasma membrane; IC.  
 DR GO; GO:0005624; C:membrane fraction; IDA.  
 DR GO; GO:0004969; P:histamine receptor activity; IDA.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR Pfam; PF00001; 7cm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PRINTS; PR01726; HISTAMINEH4R.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 KM G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 391 AA; 44248 MW; 59EC73CB5214C5E0 CRC64;

Query Match 61.1%; Score 1244; DB 2; Length 391;  
 Best Local Similarity 62.8%; Pred. No. 5.1e-76;  
 Matches 246; Conservative 43; Mismatches 99; Indels 4; Gaps 3;

QY 1 MANNST-IALTSTIKISLTFLMSLAIAMGNVVIILAFIVDRILRRHSNYFFNLAI 59  
 DB 1 MSESNTGILPPAAQVPLAFMSSFAFIMGVNAVILAFVDRILRRHSNYFFNLAI 60  
 QY 60 DEFVGAIAPIPIPSLSLTWTSGKQACVFWLITDYLLCTASVYNYVILSYDRYQSVNAV 119  
 DB 61 DELVGLISIPYIPHLFNMNFGSGICMFWLITDYLLCTASVYNYVILSYDRYQSVNAV 120  
 QY 120 WYRAQSGTWKTIATQWAVWIFSPMTNGPMILISDSWNSST--ECEPGFLKKWYFALPT 177  
 DB 121 SYRAQHTGIMKIYVQWVAVWILAFVNGMILASDSWKSTTKCEPFPVETWYIILTT 180  
 QY 178 SLLEFLIPILVAYPSAHITWYSLWKREKLSRCLSHVLPDSSSSSDHGHSCRODPSRAT 237  
 DB 181 MLLEFLIPVIVAVYFVQIYWSLWKRRALSRCPSHAGF-STTSSSAGHILHAGVACRTS 239  
 QY 238 LPARETTSLGSDSRKSSILPSIRAYKNSNVIAKMGFLSHDSIALOOREHIELEPR 297  
 DB 240 NGLESASASRHSSEPRKSSILVSRITMNSITAFKQSPWRSALRQREYAEILR 299  
 QY 298 ARKLAKSLAILLAAPAIQWAPYSLTVIYSPFPERNLTKSTWYHTAFMLQWNSFVNPL 357  
 DB 300 GRKLARSLAILLSAPAIQWAPYCLFTIVLSTYPRTRPSVWYSLAFMLQWNSFVNPL 359  
 QY 358 YPLCHRFQKAFKILPVRROSTPPHNSIST 389  
 DB 360 YPLCHRRFQKAFWKILCVTKQPALSONQSVSS 391

## RESULT 5

Q91ZY1 PRELIMINARY; PRT; 391 AA.  
 AC Q91ZY1;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Histamine H4 receptor.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 EMBL; AF35860; AK97381.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR Pfam; PF00001; 7cm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.

DR PRINTS; PR01726; HISTAMINEH4R.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KM G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 391 AA; 44023 MW; C707BA6B39CFED41 CRC64;

Query Match 60.7%; Score 1235.5; DB 2; Length 391;  
 Best Local Similarity 61.4%; Pred. No. 1.9e-75;  
 Matches 239; Conservative 46; Mismatches 101; Indels 3; Gaps 2;

QY 3 ANNSTIALTSIKISLTFLMSLAIAMGNVVIILAFIVDRILRRHSNYFFNLAIADPF 62  
 DB 4 SNGTDVLPRLTQVPPAFMSSLAFAITTGNAVILAFVADRILRRHSNYFFNLAIADPF 63  
 QY 63 VGAIAPIPIPSLSLTWTSGKQACVFWLITDYLLCTASVYNYVILSYDRYQSVNAWYR 122  
 DB 64 VGVISIPYIPIHTLFLNMNFGSGICMFWLITDYLLCTASVYNYVILSYDRYQSVNAWYR 123  
 QY 123 AQHSGTWKTIATQWAVWIFSPMTNGPMILISDSWNSST--ECEPGFLKKWYFALPTSL 180  
 DB 124 AQHTGILKIYVQWVAVWILAFVNGMILASDSWKSTTKCEPFPVETWYIILTAFL 183  
 QY 181 EFLIPILVAYPSAHITWYSLWKREKLSRCLSHVLPDSSSSSDHGHSCRODPSRATPA 240  
 DB 184 EFLFVSLVYFVQIYWSLWKRGSLSRCPSHAGFIA-TSSRGTSHSRRTGLACRTSLPG 242  
 QY 241 RRETASLGSDDRKSSILPSIRAYKNSNVIAKMGFLSHDSIALOOREHIELEPR 300  
 DB 243 LKEPAASLHSEPRKSSILVSRITMNSITAFKQSPWRSALRQREYAEILR 302  
 QY 301 LAKSLAILLAAPAIQWAPYSLTVIYSPFPERNLTKSTWYHTAFMLQWNSFVNPL 360  
 DB 303 LARSLAILLSAPAIQWAPYCLFTIVLSTYRGERPKSIWYSIAFMLQWNSILNPLVPL 362  
 QY 361 CHKRFQKAFKILPVRROSTPPHNSIST 389  
 DB 363 CHRRFQKAFWKILCVTKQPALSONQSVSS 391

## RESULT 6

Q8WNV9 PRELIMINARY; PRT; 390 AA.  
 AC Q8WNV9;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Histamine H4 receptor.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Splicein;  
 RX MEDLINE=22015261; PubMed=12020829; DOI=10.1016/S0167-4781(02)00236-1;  
 RA Oda T., Matsumoto S., Masuno Y., Takasaki J., Matsumoto M.,  
 RA Kamohara M., Saito T., Ohishi T., Soga T., Hiyama H., Matsushime H.,  
 RA Furuchi K.;  
 RT "cDNA cloning and characterization of porcine histamine H4 receptor.";  
 RL Biochim. Biophys. Acta 1575:135-138(2002).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 EMBL; AB053300; BAB83078.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR Pfam; PF00001; 7cm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PRINTS; PR01726; HISTAMINEH4R.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KM G-protein coupled receptor; Receptor; Transmembrane.

SQ SEQUENCE 390 AA; 44483 MW; BC8FD363A6F4AD3F CRC64;  
Query Match 60.0%; Score 1221.5; DB 2; Length 390;  
Best Local Similarity 62.1%; Pred. No. 1.7e-74;  
Matches 242; Conservative 45; Mismatches 92; Indels 11; Gaps 4;  
QY 4 NNSTIALTSIKISLTFLMSLAIAIMGNVAVILAFVDRNLHRNSNYFLNLAIADFFV 63  
DB 8 NNTPLPLNT-RIMLALFLMSLAIVLGNVAVILAFVDRNLHRNSNYFLNLAIADFFV 66  
QY 64 GAIAIPLYIPSSITVTSGKQACVFWLITDYLLCTASVYIVLISYDRYQSVNAWYRA 123  
DB 67 GVISIPLYIPHTLFFKWKLEEDNICAFWLIIDYLLCTASVYIVLISYDRYQSVNAWYRA 126  
QY 124 QHSGTKINTQWAVVIFSPMTGPMILISDSQNSTTECEPEFLKKYFALPTSLLEFL 183  
DB 127 QHTGIKIVLAWGVAVLAFVGPVILVSEAKQKQKQDEPEFLKEMVLAITLFEEL 186  
QY 184 IPIILVAFSAHIYMSLMKREKLSRCLSH---PVLPSDSSSDHGHSGRQDPSRATLP 239  
DB 187 APVLVAVYFNLYYMSLMKRGHLSRQSHGGLTPV-----SSGSMGHSFRCGLFSTSL 241  
QY 240 ARKETTASIGSDKSRKSSILPSIRAYKQSNVIASKMGFLSHSDSLAQREHIEFLRAR 299  
DB 242 DPKEAASLSHSEBRPRKSTLMFSLRT-RMSSLTASNMGFLSHSDSLAHQKEHIELRAR 300  
QY 300 KLAKSIALIILAAATCMAPSLTIVYSPFPEENLTKSTYHTAFWLQWNSVNFPLP 359  
DB 301 KLAKSIALIILGVAVIACWAPSLITITRSVYPTNPSTAVYKPAFWLQWNSCVNPLYP 360  
QY 360 LCHKRFQKAFKILPVROSTPPHNSIST 369  
DB 361 LCHKRFQKAFKILPVROSTPPHNSIST 390  
RESULT 7  
HH3R\_CAVPO STANDARD; PRT; 445 AA.  
AC 09J135; 09J136;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Histamine H3 receptor (HH3R).  
GN Name=HRH3;  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
OX NCBI\_TaxId=10141;  
RN 11  
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).  
RX TISSUE=Brain;  
RX MEDLINE=20218440; PubMed=10757514;  
RA Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Pillot C.,  
RA Cochois V., Schwab J.-C., Arrang J.-M.;  
RT Cloning and cerebral expression of the guinea pig histamine H3  
RT receptor: evidence for two isoforms.";  
RT NeuroReport 11:755-759(2000).  
RL  
CC -1- FUNCTION: The H3 subclass of histamine receptors could mediate the  
CC histamine signals in CNS and peripheral nervous system. Signals  
CC through the inhibition of adenylyl cyclase and displays high  
CC constitutive activity (spontaneous activity in the absence of  
CC agonist).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long; Synonyms=H3L;  
CC IsoId=09J135-1; Sequence=Displayed;  
CC Name=Short; Synonyms=H3S;  
CC IsoId=09J135-2; Sequence=VSP\_001880;  
CC -1- TISSUE SPECIFICITY: Expressed widely and abundantly throughout the  
CC brain. Highly expressed in discrete neuronal populations such as  
CC pyramidal cells in cerebral cortex or cerebellar Purkinje cells.  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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CC -----  
DR EMBL; AF267537; AAF78947.1; -;  
DR EMBL; AF267538; AAF78950.1; -;  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR003980; H3\_receptor.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PRINTS; PR01471; HISTAMINEH3R.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KM Alternative splicing; G-protein coupled receptor; Glycoprotein;  
KW Transmembrane.  
FT DOMAIN 1 40 Extracellular (Potential).  
FT TRANSMEM 41 61 Potential.  
FT DOMAIN 62 71 Cytoplasmic (Potential).  
FT TRANSMEM 72 92 Potential.  
FT DOMAIN 93 109 Extracellular (Potential).  
FT TRANSMEM 110 130 Potential.  
FT DOMAIN 131 157 Cytoplasmic (Potential).  
FT TRANSMEM 158 176 Potential.  
FT DOMAIN 179 197 Extracellular (Potential).  
FT TRANSMEM 198 218 Potential.  
FT DOMAIN 219 359 Cytoplasmic (Potential).  
FT TRANSMEM 360 380 Potential.  
FT DOMAIN 381 398 Extracellular (Potential).  
FT TRANSMEM 399 419 Potential.  
FT DOMAIN 420 445 Cytoplasmic (Potential).  
FT CARBOHYD 11 24 Poly-Ala.  
FT DOMAIND 20 11 N-linked (GlcNAc...) (Potential).  
FT VARSPIC 276 305 Missing (in isoform short).  
SQ SEQUENCE 445 AA; 48734 MW; BAE206A3887189A0 CRC64;  
Query Match 34.0%; Score 693; DB 1; Length 445;  
Best Local Similarity 37.4%; Pred. No. 7.8e-39;  
Matches 160; Conservative 67; Mismatches 139; Indels 62; Gaps 11;  
QY 3 ANNSTIALTSIKISLTFLMSLAIAIMGNVAVILAFVDRNLHRNSNYFLNLAIADFF 62  
DB 27 ARTFSAATYAV---LAAALMALIVATVLCNALVMAFVADSSILRTQNNFFLNLAISDFL 83  
QY 63 VGAIATPLTIPSLT-YMTSGKQACVFWLITDYLLCTASVYIVLISYDRYQSVNAWY 121  
DB 84 VGVFCILPVLPVYLTGRMTFGKCLMLVVDLITSSVFNVLISYDRPLSTYRAVS 143  
QY 122 RAQHSCTWIAQWAVVIFSPMTGPMILISDSQ-----NSTTE--CEPGFLKKYFA 174  
DB 144 RAQGGTTRAAVAKMVLAVLAFVGPVILVSEAKQKQKQDEPEFLKEMVLAITLFEEL 200  
QY 175 LPTSLLEFLIPIILVAFSAHIYMSLMKREKLSRCLSHPVLPSSSS----- 221  
DB 201 ITASTLEFPTPLPSVTFNLSIYLNQRTLRLLDGAAGAGDPPLPEAQSSPPQPPPG 260  
QY 222 -----SDHSGSRQDPSRATLPARKETTASIGSDKSRK 256  
DB 261 WGCWPKGQSEPHLRHYGVGAEPGAEALAGGSGAASSTSSGSSSRKTERPR-- 318  
QY 257 SSLPSIRAYKQSNVIASKMGFLSHSDSLAQREHIEFLRARLKAKSLAIIILAAFAICW 316  
DB 319 -SLKSGSKSASLSLEKMKWVSQ-----ITQR--FRLSRDKVAKSLAIIIVSIGLCW 371  
QY 317 APYSLTIVYSPFPEENLTKSTYHTAFWLQWNSVNFPLPCHKRFQKAFKILPVR 376  
DB 372 APYTLMIIRAC-HGHCVDPDYETSFWLWANSVNVNPLVPLCHYSFRRAFTKLCPO 430

OY 377 ROSTEPHN 384  
 :  
 DB 431 KLVQPHS 438  
  
 RESULT 8  
 H3R3\_HUMAN STANDARD; PRT; 445 AA.  
 AC Q9Y5N1; O9GZK2; O9H4K8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Histamine H3 receptor (H3R) (G protein-coupled receptor 97).  
 GN Name=HRH3; Synonyms=GPRC97;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCB1\_taxonomy606;  
 RN (1)  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Thalamus;  
 RX MEDLINE=99279519; PubMed=10347254;  
 RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,  
 RT Huvar A., Jackson W.R., Eriander M.G.;  
 RT "Cloning and functional expression of the human histamine H3  
 RT receptor.";  
 RT Mol. Pharmacol. 55:1101-1107(1999).  
 RN (2)  
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.  
 RX MEDLINE=20568725; PubMed=1119334; DOI=10.1006/dbic.2000.4008;  
 RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;  
 RT "Molecular cloning and characterization of a new human histamine  
 RT receptor, HRH3.";  
 RT Biochem. Biophys. Res. Commun. 279:615-620(2000).  
 RN (3)  
 RP SEQUENCE FROM N.A. (ISOFORMS 1, 3, 4, 5, 6 AND 7).  
 RC TISSUE=Thalamus;  
 RX MEDLINE=21181559; PubMed=11284713; DOI=10.1042/0264-6021.3550279;  
 RA Cogde F., Guenlin S.-P., Audinat E., Renouard-Try A., Beauverger P.,  
 RT Macia C., Ouvre C., Nagel N., Rigue H., Boulin J.A., Gallizzi J.-P.;  
 RT "Genomic organization and characterization of splice variants of the  
 RT human histamine H3 receptor.";  
 RT Biochem. J. 355:279-288(2001).  
 RN (4)  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME  
 VAL-280.  
 RC TISSUE=Blood;  
 RX MEDLINE=21953383; PubMed=11956964; DOI=10.1007/s007020200036;  
 RA Wiedemann P., Boenisch H., Oerters F., Brunes M.;  
 RT "Structure of the human histamine H3 receptor gene (HRH3) and  
 RT identification of naturally occurring variations.";  
 RT J. Neural Transm. 109:443-453(2002).  
 RN (5)  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC "Cloning and functional expression of the human histamine H3  
 RT receptor.";  
 RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN (6)  
 RP SEQUENCE FROM N.A. (ISOFORM 1)  
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/41465a1;  
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagunley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Gardner C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A.G., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Lehevaeslatho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McElroy K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel A., Pearce T.A.V., Peck A.I.,  
 RA Philimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 CC -1- FUNCTION: The H3 subclass of histamine receptors could mediate the  
 CC histamine signals in CNS and peripheral nervous system. Signals  
 CC through the inhibition of adenylyl cyclase and displays high  
 CC constitutive activity (spontaneous activity in the absence of  
 CC agonist). Agonist stimulation of isoform 3 neither modified  
 CC adenylyl cyclase activity nor induced intracellular calcium  
 CC mobilization.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1;  
 CC IsoId=Q9Y5N1-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9Y5N1-2; Sequence=VSP\_001886;  
 CC Name=3; Synonyms=H3S;  
 CC IsoId=Q9Y5N1-3; Sequence=VSP\_001885;  
 CC Name=4;  
 CC IsoId=Q9Y5N1-4; Sequence=VSP\_001881;  
 CC Name=5;  
 CC IsoId=Q9Y5N1-5; Sequence=VSP\_001882;  
 CC Name=6;  
 CC IsoId=Q9Y5N1-6; Sequence=VSP\_001883;  
 CC Name=7;  
 CC IsoId=Q9Y5N1-7; Sequence=VSP\_001884;  
 CC -1- TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the  
 CC greatest expression in the thalamus and caudate nucleus. The  
 CC various isoforms are mainly coexpressed in brain, but their  
 CC relative expression level varies in a region-specific manner.  
 CC Isoforms 3 and 7 are highly expressed in the thalamus, caudate  
 CC nucleus and cerebellum while isoforms 5 and 6 show a poor  
 CC expression. Isoforms 5 and 6 show a high expression in the  
 CC amygdala, substantia nigra, cerebral cortex and hypothalamus.  
 CC Isoform 7 is not found in hypothalamus or substantia nigra.  
 CC -1- DISEASE: Defects in HRH3 are a cause of Shy-Drager syndrome  
 CC [MIM:146500]. This syndrome is characterized by orthostatic  
 CC hypotension, bladder and bowel incontinence, anhidrosis, iris  
 CC atrophy, amyotrophy, ataxia, rigidity and tremor.  
 CC -1- MISCELLANEOUS: Does not bind to cimetidine and triptolidine. Shows  
 CC modest affinity for thioflavine, imetit, N-alpha-methylhistamine  
 CC and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to  
 CC idopropoxyfan while isoforms 1 and 3 bind it with high affinity.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, AF140538; AAD38151.1; -  
 CC EMBL, AB045369; BAB20090.1; -  
 CC EMBL, AB019000; BAB17030.1; -  
 CC EMBL, AJ296652; CACS1025.1; -  
 CC EMBL, AJ278250; CACS9434.1; -  
 CC EMBL, AL078633; CAC04014.1; -

DR EMBL; AF363791; AAK50040.1; -.  
 DR Genew; HGNC:5184; HRH3.  
 DR MIM; 146525; -.  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO; GO:0004969; F: histamine receptor activity; TAS.  
 DR GO; GO:0007187; P: G-protein signaling, coupled to cyclic nucl. .; TAS.  
 DR GO; GO:0007269; P: neurotransmitter secretion; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR003980; H3\_receptor.  
 DR Pfam; PF00001; 7tm\_1, 1.  
 DR PRINTS; PRO0237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_FL\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECPT\_FL\_2; 1.  
 DR Alternative splicing; Disease mutation; G-protein coupled receptor;  
 KW Glycoprotein; Transmembrane.  
 FT DOMAIN 1 39  
 FT TRANSMEM 40 60  
 FT DOMAIN 61 70  
 FT TRANSMEM 71 91  
 FT DOMAIN 92 108  
 FT TRANSMEM 109 129  
 FT DOMAIN 130 156  
 FT TRANSMEM 157 177  
 FT DOMAIN 178 196  
 FT TRANSMEM 197 217  
 FT DOMAIN 218 359  
 FT TRANSMEM 360 380  
 FT TRANSMEM 381 395  
 FT TRANSMEM 396 416  
 FT DOMAIN 417 445  
 FT DOMAIN 250 256  
 FT DOMAIN 292 298  
 FT CARBOHYD 11 11  
 FT VARSPLIC 85 98  
 FT VARSPLIC 197 315  
 FT VARSPLIC 227 342  
 FT VARSPLIC 234 263  
 FT VARSPLIC 274 353  
 FT VARSPLIC 445 445  
 FT VARIANT 280 280  
 FT CONFLICT 19 19  
 FT SEQUENCE 445 AA; 48671 MW; 2ACF7440FBB95B6C CRC64;

Query Match 33.9%; Score 689.5; DB 1; Length 445;  
 Best Local Similarity 37.3%; Pred. No. 1.3e-38;  
 Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;

QY 3 ANNSTALTSIKISLTFLMSLAIATMLGNVVIIAFYDRNRHRSNYFFLNLAIADFF 62  
 DB 26 ARGFSAAWTA--LALMALIIVATVGNALVMAFVADSLRQNNFFLNLAIADFF 82  
 QY 63 VGAIAPLPIPSLT-YMTSGQACVFMILTYLCTASVYNIVLISYRQSVSAWVY 121  
 DB 83 VGAFCLPIVPPVLTGRMTFGRLCKMLVVDLLCTSSAFNVLISYDRFSLVTRAVSY 142  
 QY 122 RAQSGTWIATQAVAVWIFSPMTNGPMILISDSWQ---NSTTE--CEPGFLKKMYA 174  
 DB 143 RAQGGTTRAVAKMLVWVLAFLVGPAIL---SWEYLSGGSSIPGHCAEFYMYWYL 199  
 QY 175 LPTSLLEPLPIILVAVFSAHYWSLWKREK---SRCLSHVLPDSGSSS----- 222  
 DB 200 ITASTLEFPTPLSLVTFNLSIYLNIOKRTRLDGAAREAGPEPPPEAOPSPPPPGCW 259

QY 223 -----DHGSCRODPDSR-----ATL-----PARKETASIGSDK 252  
 DB 260 GCMQKHGEAM---PLHRYGVEAAVGAAGETLIGCGGGGGSVASPTSSGSSSNGTGR 316  
 QY 253 SRRKSLSPISRAYKSNVIAKMGFLSHSDSLAQORHIELFRARKLAKSLAIIILAAF 312  
 DB 317 PR---SLKRGSPKSPASASLEKRMKVQSFT-----ORFLSRDRKVAKSLAVVSIF 367  
 QY 313 AICMAPYSLTYVIYSPFERNLTKSTWHTAFMLQWFSFNVPYPLCHKPFQKAFKI 372  
 DB 368 GLCMAPYTLMLTIKAC-HGICVPDIWYETSFMLMANSVAVNPYPLCHSHFRRAFTKL 426  
 QY 373 LPEVRQSTPPHN 384  
 DB 427 LCPQKLKIQPHS 438

RESULT 9  
 ID 0865E1 PRELIMINARY; PRT; 445 AA.  
 AC 0865E1;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Histamine receptor H3.  
 GN Name=HRH3;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yao B.B., Sharma R., Casar S., Esbenshade T.A., Hancock A.A.;  
 RL Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AY231164; A063757.1; -.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0004969; F: histamine receptor activity; IEA.  
 DR GO; GO:0004872; F: receptor activity; IEA.  
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR003980; H3\_receptor.  
 DR Pfam; PF00001; 7tm\_1, 1.  
 DR PRINTS; PRO0237; GPCRHHODPSN.  
 DR PROSITE; PRO1471; HISTAMINEHR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_FL\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECPT\_FL\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 445 AA; 48591 MW; E79440A4EC09CA8C CRC64;

Query Match 33.8%; Score 688.5; DB 2; Length 445;  
 Best Local Similarity 37.8%; Pred. No. 1.6e-38;  
 Matches 161; Conservative 66; Mismatches 142; Indels 57; Gaps 12;

QY 3 ANNSTALTSIKISLTFLMSLAIATMLGNVVIIAFYDRNRHRSNYFFLNLAIADFF 62  
 DB 26 ARGFSAAWTA--LALMALIIVATVGNALVMAFVADSLRQNNFFLNLAIADFF 82  
 QY 63 VGAIAPLPIPSLT-YMTSGQACVFMILTYLCTASVYNIVLISYRQSVSAWVY 121  
 DB 83 VGAFCLPIVPPVLTGRMTFGRLCKMLVVDLLCTSSAFNVLISYDRFSLVTRAVSY 142  
 QY 122 RAQSGTWIATQAVAVWIFSPMTNGPMILISDSWQ---NSTTE--CEPGFLKKMYA 174  
 DB 143 RAQGGTTRAVAKMLVWVLAFLVGPAIL---SWEYLSGGSSIPGHCAEFYMYWYL 199  
 QY 175 LPTSLLEPLPIILVAVFSAHYWSLWKREK---SRCLSHVLPDSGSSS----- 222  
 DB 200 ITASTLEFPTPLSLVTFNLSIYLNIOKRTRLDGAAREAGPEPPPEAOPSPPPPGCW 259

Oy	223	-----DHGSC--CODPSRATLPARKET-----TASLGDK--SPRKS	252
Db	260	GCWQGHGEMPLHRYGVVEAAGAAGETALGCGGGGSAAPTSSSGSSNGTERPPS	319
Oy	259	LLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELPARKLAKSLATILAAFAICWAP	318
Db	320	LKRGSKPSSASLSEKRMKGVQSFT-----GRFLSRDKRVAKSLAVIVSIFGLCWAP	373
Oy	319	YSLTVIVSYSPFERNLTKSTWYHTAWLOWFNFSFVNPFLPYPLCHKPQKAFKILPVRRQ	378
Db	374	YTLMTITIRAC-HGHCVPDPWYETSFPLLMANSANVPVLPYLCHHSFRRAFTYLLCPQKL	432
Oy	379	STPPHN	384
Db	433	KIQPHS	438
RESULT	10		
H3R	RAT		
ID	H3R	RAT	STANDARD: PRT: 445 AA.
AC	O9QYN8; O9QYNS; O9QYN7; O9QYN9;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Histamine H3 receptor (H3R).		
GN	Name=H3h3.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSE=hypothalamus;		
RC	MEDLINE=20330707; PubMed=10869375;		
RA	Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;		
RT	"Cloning of rat histamine H3 receptor reveals distinct species		
RT	pharmacological profiles."		
RL	J. Pharmacol. Exp. Ther. 293:771-778(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RC	TISSE=striatum;		
RC	MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;		
RA	Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,		
RA	Stark H., Schumack W., Genellin C.R., Schwartz J.-C., Arrang J.-M.;		
RT	"High constitutive activity of native H3 receptors regulates histamine		
RT	neurons in brain."		
RL	Nature 408:860-864(2000).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1, 2, 3 AND 4).		
RA	Iedani H., Takimura T., Nakamura T., Ohta M.;		
RT	"Cloning of a novel G protein-coupled receptor."		
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBD databases.		
RN	[4]		
RP	TISSE SPECIFICITY.		
RX	MEDLINE=99278519; PubMed=10347254;		
RA	Lovenberg T.W., Roland B.L., Wilson S.-J., Jiang X., Pyati J.,		
RA	Huvar A., Jackson M.R., Erlander M.G.;		
RT	"Cloning and functional expression of the human histamine H3		
RT	receptor."		
RL	Mol. Pharmacol. 55:1101-1107(1999).		
CC	-I- FUNCTION: The H3 subclass of histamine receptors could mediate the		
CC	histamine signals in CNS and peripheral nervous system. Signals		
CC	through the inhibition of adenylyl cyclase and displays high		
CC	constitutive activity (spontaneous activity in the absence of		
CC	agonist).		
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-I- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=4;		
CC	Comment=Additional isoforms seem to exist;		
CC	Name=1; Synonyms=H3L;		
CC	Isoid=O9QYN8-1; Sequence=Displayed;		
CC	Name=2; Synonyms=H3S;		
CC	Isoid=G9QYN8-2; Sequence=VSP_001887;		

[illegible]

QY 63 VQAIAIPLYIPSSLT-YMTSGKQACVFMLITDYLCTASVYNIIVLISYDRYOSVSNVWY 121  
 DB 83 VQAFCIPLYVYPVLTGRMTFGRGLCKLMLVVDLTCASSVFNIIVLSYDRFLSVTAIVG 142  
 QY 122 RAQHSCTKIAIOMVAWVIFSEMTNGPMILISDSWQ-----NSTTE--CEPGFLKMYRA 174  
 DB 143 RAQOGDTRAVRKMAVWVLAFLYGPALV---SWEYLSGSGSIPGHCYAEFFVWYFL 199  
 QY 175 LPTSLIEFLIPILIVAFSAHIYMSLMKREKL---SRCLSHPLVLPDSSSS----- 222  
 DB 200 ITASTLEFPTPLSVTFPFLSLIYLNIOKRTRLDGRAGREPPPDAPSPPPAPSCW 259  
 QY 223 -----DHGHSCHRODPDSR-----ATLPARKETTASIGSPK 252  
 DB 260 GCMFKXHGEM---PLHRYGVGEAGPGVEAGEAALGGSGGGAALPTSSSSSSSGCTER 316  
 QY 253 SRKSSLLPSIRAYKNSVNIASIKMGFLSHSDSLAQOREHIELFRARKLAKSLAIIILAA 312  
 DB 317 PR---SLKRGSKPSASASALEKMKVWSQS---ITQR--FRLSRDKVAKSLAIIIVSIF 367  
 QY 313 AICWAPYSLTIVYISFPPERNLTKSTWYHTAFWLCWPNFVNPFLYPLCHKRQKAFKI 372  
 DB 368 GLCWAPYTLTLMITRAACHGRCI-PDYWYETSWFLWANSVAVNPVLYPLCHYSFRRAFTYL 426  
 QY 373 LPVRROSTEPH 383  
 DB 427 LCPQKXKXQPH 437

RESULT 11  
 HH3R MOUSE STANDARD; PRT; 445 AA.  
 AC PS8406;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Histamine H3 receptor (HH3R).  
 GN Name=Hh3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxId=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1;  
 RA Coge F., Rigue H., Leveacher B., Leopold O., Guenin S.-P., Boutin J.A.,  
 RA Gallizzi J.-P.;  
 RT "Cloning of mouse histamine H3 receptor."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC - FUNCTION: The H3 subclase of histamine receptors could mediate the  
 histamine signals in CNS and peripheral nervous system. Signals  
 through the inhibition of adenylylate cyclase and displays high  
 constitutive activity (spontaneous activity in the absence of  
 agonist) (By similarity).  
 CC - SUBCELLULAR LOCATION: Integral membrane protein.  
 CC - SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; AY044153; AA072406.1; -  
 CC MGD; MGI:2139279; Hm3.  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC InterPro: IPR003980; H3\_receptor.  
 CC Pfam; PF00001; 7tm\_1; 1.  
 CC PRINTS; PR00237; GPCRHDOPSN.  
 CC PRINTS; PR01471; HISTAMINEH3.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECPT\_FL\_1; 1.

DR PROSITE, PS0262; G\_PROTEIN\_RECPT\_FL\_2; 1.  
 KM G-protein coupled receptor; Glycoprotein; Transmembrane.  
 FT DOMAIN 1 39  
 FT TRANSMEM 40 60  
 FT DOMAIN 61 70  
 FT TRANSMEM 71 91  
 FT DOMAIN 92 108  
 FT TRANSMEM 109 129  
 FT DOMAIN 130 156  
 FT TRANSMEM 157 177  
 FT DOMAIN 178 196  
 FT TRANSMEM 197 217  
 FT DOMAIN 218 359  
 FT TRANSMEM 360 380  
 FT DOMAIN 381 396  
 FT TRANSMEM 397 417  
 FT DOMAIN 418 445  
 FT CARBOHYD 20 23  
 FT CARBOHYD 11 11  
 SQ SEQUENCE 445 AA; 48541 MW; B8D406E29E1F3C5F CRC64;  
 Query Match 33.4%; Score 679.5; DB 1; Length 445;  
 Best Local Similarity 37.4%; Pred. No. 6,4e-38;  
 Matches 161; Conservative 65; Mismatches 136; Indels 69; Gaps 13;

QY 3 ANNSTIALTSIKISLTFELMSLLAIAIMGNVVYLAIFYDRNLRHNSYFNLAIADPF 62  
 DB 26 ANGSANMTAV---LALMALILVATVGNALVWLAFFVADSSLRTONNFFLNLAIADFL 82  
 QY 63 VQAIAIPLYIPSSLT-YMTSGKQACVFMLITDYLCTASVYNIIVLISYDRYOSVSNVWY 121  
 DB 83 VQAFCIPLYVYPVLTGRMTFGRGLCKLMLVVDLTCASSVFNIIVLSYDRFLSVTAIVG 142  
 QY 122 RAQHSCTKIAIOMVAWVIFSEMTNGPMILISDSWQ-----NSTTE--CEPGFLKMYRA 174  
 DB 143 RAQOGDTRAVRKMAVWVLAFLYGPALV---SWEYLSGSGSIPGHCYAEFFVWYFL 199  
 QY 175 LPTSLIEFLIPILIVAFSAHIYMSLMKREKL---SRCLSHPLVLPDSSSS----- 222  
 DB 200 ITASTLEFPTPLSVTFPFLSLIYLNIOKRTRLDGRAGREPPPDAPSPPPAPSCW 259  
 QY 223 -----DHGHSCHRODPDSR-----ATLPARKETTASIGSPK 252  
 DB 260 GCMFKXHGEM---PLHRYGVGEAGPGVEAGEAALGGSGGGAALPTSSSSSSSGCTER 316  
 QY 253 SRKSSLLPSIRAYKNSVNIASIKMGFLSHSDSLAQOREHIELFRARKLAKSLAIIILAA 312  
 DB 317 PR---SLKRGSKPSASASALEKMKVWSQS---ITQR--FRLSRDKVAKSLAIIIVSIF 367  
 QY 313 AICWAPYSLTIVYISFPPERNLTKSTWYHTAFWLCWPNFVNPFLYPLCHKRQKAFKI 372  
 DB 368 GLCWAPYTLTLMITRAACHGRCI-PDYWYETSWFLWANSVAVNPVLYPLCHYSFRRAFTYL 426  
 QY 373 LPVRROSTEPH 383  
 DB 427 LCPQKXKXQPH 437  
 RESULT 12  
 06ZM33 PRELIMINARY; PRT; 473 AA.  
 AC 06ZM33;  
 DT 05-JUL-2004 (TEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
 DE SI:b23462.4 (Novel protein similar to human histamine receptor H3  
 (HRH3)).  
 GN Name=si:rp71-3462.4; Synonyms=SI:b23462.4;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxId=7955;

[1]  
 RN SEQUENCE FROM N.A.  
 RP Tracey A.;  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBS databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL, AL928906; CAB49238.1; -;  
 DR ZFIN, ZDB-GENE-040724-204; sl:fp71-3492.4.  
 DR GO, GO:0016021; C:integral to membrane; IEA.  
 DR GO, GO:0004969; F:histamine receptor activity; IEA.  
 DR GO, GO:0004872; F:receptor activity; IEA.  
 DR GO, GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO, GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro, IPR002276; GPCR\_Rhodopsn.  
 DR InterPro, IPR003980; H3\_receptor.  
 DR Pfam, PF00001; 7tm\_1; 1.  
 DR PRINTS, PR00237; GPCR\_RHODOPSIN.  
 DR PRINTS, PR01471; HISTAMINEH3.  
 DR PROSITE, PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE, PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 KW SEQUENCE 473 AA; 53506 MW; 032RC7C27D8C6E57 CRC64;

Query Match 32.7%; Score 666; DB 2; Length 473;  
 Best Local Similarity 37.5%; Pred. No. 5.5e-37;  
 Matches 155; Conservative 64; Mismatches 148; Indels 46; Gaps 12;

QY 12 SIKISLTFMSLAIATIMGNVVIATFVDRNLHRSNVFFLNLAIADFGAIAIPLY 71  
 DB 62 STSIFLVTMTLVATVATVGNALVILAFVVEKSLRQGNFFLNLAIADFLVGGCIPY 121  
 QY 72 IPSSLT-YWTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVNNAVYPAQHSQTWK 130  
 DB 122 IPYVLTGEWRLTGKGLKLVVDYMLCTASVFNIVLISFDRQSVTKAVSYRCQKGTXD 181  
 QY 131 IATQWVAWIFEFMTNGPMILISDSQNT-----TCEBGLKMWFAIPSLILETL 183  
 DB 182 AVLKMLCWLAAFLVLYGPAIL---SWEHLTGSGVVPDGCYAEFFNWYFLMTASTVERF 238  
 QY 184 IPIILVAYSAAIYMSLMREKLS-----RCLSHPVLPSSSSSDHSGCRQDPDR- 235  
 DB 239 TFFISVTYNLSITINIRRCAMREQPTVYLLRSKMPFLGAGDVQRTFPRVPEBSIV 298  
 QY 236 ATLPAKKE-----TASL-----GSDKSRKSSL--LPSIRAYKNSNVIA--SKMGF 278  
 DB 259 ADLARSRCRLSAKAVSAEFNGRQGRDSTLADPLQV--EERILLASEAQPHY 356  
 QY 279 LSHS-----DSLALQREHTELPRARLAKSLAILLAFAICWAPYSLTIVISFFPE 331  
 DB 357 VDHSAQPHRRPDMVASLANRFLSLDKKVAKSLAVICVFGLCWAPYLLMIIRAAC-H 415  
 QY 332 RMLTSTWYHTAFWLMQWFSFVNPFLYPLCHKRFOKAFKILPVRRQSTPPHN 384  
 DB 416 GQCVGHVLYEISFWLIMINSINPILYPLCHSSFKRAFSKLLCPSTKTIQPON 468

## RESULT 13

Q8WY01 PRELIMINARY; PRT; 365 AA.  
 AC Q8WY01;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Histamine H3 receptor isoform 2.  
 GN Name=HRH3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN NCBI\_Taxid=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=hippocampus;  
 RA Wellendorp P., Goodman M.W., Birstein E.S., Nash N.R., Brann M.R.,

RA Weiner D.M.;  
 RT "Molecular Cloning and Characterization of Functionally Distinct  
 RT Isoforms of the Human Histamine H3 Receptor."  
 RL Neuropharmacology 0:0-0(2002).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL, AF321911; AAL71812.1; -;  
 DR GO, GO:0016021; C:integral to membrane; IEA.  
 DR GO, GO:0004969; F:histamine receptor activity; IEA.  
 DR GO, GO:0004872; F:receptor activity; IEA.  
 DR GO, GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO, GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR Pfam, PF00001; 7tm\_1; 1.  
 DR PRINTS, PR00237; GPCR\_RHODOPSIN.  
 DR PRINTS, PR01471; HISTAMINEH3.  
 DR PROSITE, PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE, PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 KW SEQUENCE 365 AA; 40609 MW; D7BB32042464CB35 CRC64;

Query Match 32.2%; Score 655.5; DB 2; Length 365;  
 Best Local Similarity 36.7%; Pred. No. 2.2e-36;  
 Matches 146; Conservative 60; Mismatches 111; Indels 81; Gaps 10;

QY 3 ANNSTIALTSIKISLTFMSLAIATIMGNVVIATFVDRNLHRSNVFFLNLAIADFG 62  
 DB 26 ARGFSAMTAV---LAALMALIVATVGNALVILAFVADSLSLRQNNFFLNLAIADFL 82  
 QY 63 VGAIAPLYIPSSLT-YWTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVNNAVY 121  
 DB 83 VGAFCLPVTVPVYLVGRMTFGKGLKLVVDYMLCTASVFNIVLISFDRQSVTKAVSY 142  
 QY 122 RAQHSQTKIKIATQWVAWIFEFMTNGPMILISDSQNT-----NSTTE--CEBGLKMWFA 174  
 DB 143 RAQQGDTRAVRKMLVWVLAFLVLYGPAIL---SWEYLSGSGSIIEGHCYAEFFNWYFL 199  
 QY 175 LPTSLILEFLIPLLVAYSAIYMSLMREKLS-----SRCLSHPVLPSSSSSDHSG- -H 226  
 DB 200 ITASTLEFFTPPLSTFPNLSITYNICQRTTRRLDGAEEAGPEPPPEQAPSPPPPGCW 259  
 QY 227 SCRODPDRATLPARKETTAGISGDSKSRKSSSLPSIRAYKNSNVIAKMGSLSHSDSLA 286  
 DB 260 GCMQR-----GHEANP 271  
 QY 287 LQOREHIELFARKLAKSLAILLAFAICWAPYSLTIVISFFPRNLTKSTWYHTAFWL 346  
 DB 272 LH-----RKVAKSLAVIVSIFGLCWAPYLLMIIRAAC-HGHCVPDVTWYTSFWL 320  
 QY 347 QWFSFVNPFLYPLCHKRFOKAFKILPVRRQSTPPHN 384  
 DB 321 LWANAVNPVLYPLCHHSFRFAFTLLCPQKLIKIOPHS 358

## RESULT 14

Q8WX29 PRELIMINARY; PRT; 373 AA.  
 AC Q8WX29;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Histamine H3 receptor isoform 4.  
 GN Name=HRH3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN NCBI\_Taxid=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=hippocampus;  
 RA Wellendorp P., Goodman M.W., Birstein E.S., Nash N.R., Brann M.R.,  
 RA Weiner D.M.;  
 RT "Molecular Cloning and Characterization of Functionally Distinct  
 RT Isoforms of the Human Histamine H3 Receptor.";

```

RL Neuropharmacology 0:0-0(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AF321913; AAL7914.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004969; F:histamine receptor activity; IEA.
DR GO: GO:0004872; F:histamine receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOOPSN.
DR PROSITE: PR01471; HISTAMINEHR.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 373 AA; 41570 MW; PAEDFCSCAFDE9 CRC64;

Query Match 32.2%; Score 655.5; DB 2; Length 373;
Best Local Similarity 36.7%; Pred. No. 2.2e-36;
Matches 146; Conservative 60; Mismatches 111; Indels 81; Gaps 10;

QY 3 ANNSTALTSIKISLTFELKSLAIAIMLGNVVVILAFIDRNLRHSNYEFLNLATADFF 62
DB 26 AAGFSAWTAV---LALMALILIVATVLSNALVWLFVADSSLRQNNFLLNLATIDFL 82
QY 63 VCAIAIPLYIPSSLT-YWTSKQACVFWLITDYLCTASVNIIVLISYDRYSVSNVAVY 121
DB 83 VQAFICPLVYVLTGRWTFGRGLCKLWLVVDYLCTSSAFNIVLISYRFLSVTRAIVY 142
QY 122 RAQHGSTWKLATQWAVVWFSPMTNGPMILISDSWC---NSTTE-CEPGFLKKWYRA 174
DB 143 RAQCGTTRAVVRKMLVWVLAFLYGPAIL---SWEYLSGSSIPRGHCYAEFFYMWYFL 199
QY 175 LPTSLLEFLILIVAVFSAHYWSLMKREKL---SRCLSHPVLPSSSSSDHG---H 226
DB 200 ITASTLEFTFPFLSVTFEFLSTYLNIQRTRRLDGAERADAGEPPPEAOPSPPPPGCW 259
QY 227 SCROPDPSRATLPARKETTASLGSDDRKSSILPSIRAYKSNVNIASKGFLSHSDSLA 286
DB 260 GCMQK-----GHCAMP 271
QY 287 LQQRHEILFARKKLAKSLAIIILAFATCMAPYSTTVIYSPFERNLTKSTWYHTAFWL 346
DB 272 LH-----RKVAKSLAVIVSIFGLCMAPYTLIMIRAC-HGHCVPDYWYETSPWL 320
QY 347 QWFNSFVNPLYLCHKRFQKAFKLIPRRROSTPPHN 384
DB 321 IMAISAIVNPLVLYLCHHSFRRAFTKLCPQKLIKQPHS 358

RESULT 15
ID 06J9J4 PRELIMINARY; PRT; 174 AA.
AC 06J9J4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Histamine receptor H4 subtype (Fragment).
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=15123584; DOI=10.1101/gr.1891104;
RA Zhang J., Wang X., Podlana O.;
RT "Testing the chromosomal speciation hypothesis for humans and
RT chimpanzees.";
RL Genome Res. 14:845-851(2004).
DR EMBL: AY561470; RAT4508.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.

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DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR Rhodpsn.
DR InterPro: IPR008102; Histamine_recept_H4.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOOPSN.
DR PRINTS: PR01726; HISTAMINEHR.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
FT NON TER 1 1
FT NON TER 174 174
SQ SEQUENCE 174 AA; 19713 MW; 4038B74734A785F5 CRC64;

Query Match 26.3%; Score 534.5; DB 2; Length 174;
Best Local Similarity 62.4%; Pred. No. 1.5e-28;
Matches 108; Conservative 18; Mismatches 46; Indels 1; Gaps 1;

QY 206 LSRCLSHPVLPSSSSSDHGHCRCRQDPDSRATLPARKETTASLGSDDRKSSILPSIRA 265
DB 2 LSRCSHPGL-TGVSSNLCGHSGFRGLSSRRSLASAEVPASLHSERRQRKSLMPSRST 60
QY 266 YKNSNVIASKMGFLSHSDSLAQQRHEILFARKKLAKSLAIIILAFATCMAPYSTTVI 325
DB 61 KMSNSTIAKMGSFSSQSDVALHQREHVELLARRKLAKSLAIIILGVFAVCMAPYSTTVI 120
QY 326 YSFFPERNLTKSTWYHTAFWLQWFNSFVNPLYLCHKRFQKAFKLIPRRRO 378
DB 121 LSFYSATGPKSVMYRIAFWLQWFNSFVNPLYLCHKRFQKAFKLIPRRRO 173

Search completed: August 3, 2005, 01:57:01
Job time : 174 secs

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